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The Algebra of Genetic Algorithms

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Abstract

A rigorous formulation of the generalisation of schema analysis known as forma analysis is presented. This is shown to provide a direct mechanism for harnessing knowledge about a search space, codified through the imposition of equivalence relations over that space, to generate a genetic representation and operators. It is shown that a single characterisation of a space leads to a unique genetic representation, and the kinds of representations that are possible are classified and discussed. A relatively new operator, call *random assorting recombination* (RAR_w), is defined rigorously and is shown to be, in an important sense, a universal recombination operator.

1 Overview

The standard theory of genetic algorithms is based on *schema analysis* (Holland, 1975). Schema analysis operates in the representation (genotype) space and can be used provided that the chromosomes chosen are linear strings made up of a fixed number of *genes* (positions) each of which has a well-defined set of possible *alleles* (values) and provided also that any combination of alleles is permitted (so that all strings are legal). Schema analysis has been extremely fruitful in yielding insight into the operation of genetic algorithms, and has recently been extended to provide exact models with executable forms which trace the evolution of individual strings, both for infinite and finite populations (Nix & Vose, 1991; Vose & Liepins, 1991a; Whitley, 1992). Various limitations remain apparent, however, and these are discussed in section 2. As a result of these perceived limitations, various extensions and generalisations have been proposed (Goldberg & Lingle, 1985; Antonisse, 1989; Radcliffe, 1990; Vose, 1991). This paper is concerned only with the particular generalisation called *forma analysis*, which has been developed in a series of papers (Radcliffe, 1990, 1991a, 1991b, 1993, 1992a, 1992b), though the relationship between forma analysis and other generalisations is touched on in the discussion at the end of the paper (section 7). The purpose of the present paper is to define forma analysis rather more rigorously than has before been attempted and to prove certain results that have previously either been taken for granted or left open. In the process, there will also be a certain amount of "cleaning-up" of notation.

The remainder of the present section provides a relatively detailed overview of the contents of the rest of the paper. Section 2 briefly re-states the features of schema analysis that have motivated the development of forma analysis and connects the necessarily rather formal content of the body of this paper to practical problems encountered when using genetic algorithms. Its content is similar to—but less detailed than—that of Radcliffe (1992b).

Section 3 formally introduces equivalence relations, which are central to forma analysis, together with a certain amount of associated notation. Readers already familiar with equivalence relations and forma analysis may wish to proceed directly to definition 1 in section 3 after this overview. An algebra of equivalence relations is then introduced in section 4 by defining intersection for equivalence relations. The basis of the approach taken involves codifying such knowledge of the search space as is available using a set of equivalence relations (or partitions of the search space) that group together solutions whose performance might reasonably be expected to be correlated. Provided that these equivalence relations are sufficiently rich, in a sense to be defined, this then allows a genetic representation and a set of operators to be defined "automatically". To facilitate the formulation and analysis of both this representation and the operators described, appropriate definitions of *span*, *independence*, *coverage*, *orthogonality* and *basis* (in the context of equivalence relations) are then introduced, and it is formally demonstrated that orthogonality implies independence, as sense requires.

Section 5 is concerned with representation, and shows in detail the way in which a basis for a suitable set of equivalence relations over a search space can be used to generate a faithful representation of that search space, or equivalently how a useful genotype space can be generated "automatically" from a phenotype space. A precise formulation of the terms *gene* and *allele* is then provided, and this will be found to align very naturally with standard usage of these terms within the field. The important result that every set of equivalence relations contains a unique basis is then proved, which in turn shows—loosely—that each characterisation of a search space (codified through a set of equivalence relations) leads to a unique genetic representation.

Section 6 is concerned with recombination. Following similar principles to but a more formal discipline than earlier discussions of forma analysis, principles for guiding the design of recombination operators are first described, and then applied to construct a family of representation-independent operators. These principles include the notions of respect, assortment and gene transmission discussed in earlier works. Three operators are then generated, two of which—random respectful recombination (R^3) and random transmitting recombination (RTR)—have been described in some detail before, together with a rather newer operator, random *assorting* recombination (RAR). It is demonstrated that when the basis for the equivalence relations is orthogonal, (which in turn means that alleles may be independently assigned to genes) forma analysis reduces to schema analysis, and the operators discussed in this paper reduce to standard operators. This section also contains a discussion of the conditions under which the properties suggested for recombination operators are mutually compatible, and shows that RAR may be "tuned" to allow appropriate accommodation between them in cases of conflict.

The final section, section 7, is a discussion of the results presented and their interpretation. This includes consideration of linkage, disruption and the relative merits and ease of manipulating operators and representations to desired ends.

2 Motivation

The initial motivation for developing forma analysis is a consideration of the Schema Theorem (Holland, 1975) and the rôle of implicit parallelism. This theorem may be stated in a fairly general form (though assuming fitness-proportionate selection) thus:

$$\langle N_\xi(t+1)\rangle \geq N_\xi(t)\frac{\hat{\mu}_\xi(t)}{\bar{\mu}(t)}\left[1-\sum_{\omega\in\Omega}p_\omega p_\omega^\xi\right] \tag{1}$$

where

- $N_\xi(t)$ is the number of members of the population at time t that are members of a given schema ξ;

- $\hat{\mu}_\xi(t)$ is the observed fitness of the schema ξ at time t, i.e. the average fitness of all the members of the population at time t that are instances (members) of the schema ξ;
- $\bar{\mu}(t)$ is the average fitness of the whole population at time t;
- Ω is the set of genetic operators in use;
- the term $p_\omega p_\omega^\xi$ quantifies the potential disruptive effect on schema membership of the application of operator $\omega \in \Omega$;
- $\langle \cdot \rangle$ denotes an expectation value.

This theorem is fairly easily proved. It has been extended by Bridges & Goldberg (1987) (for the case of binary schemata) to replace the inequality with an equality by including terms for string gains as well as the disruption terms.

It is both a strength and a weakness of the schema theorem that it applies equally, given a representation space $\mathcal{C}$ (of "chromosomes" or "genotypes"), for a search space $\mathcal{S}$ (of "phenotypes"), whichever mapping is chosen to relate genotypes to phenotypes. Assuming that $\mathcal{S}$ and $\mathcal{C}$ have the same size, there are $|\mathcal{S}|!$ such mappings (representations) available—clearly vastly more than the size of the search space itself—yet the schema theorem applies equally to each of them. The only link between the representation and the theorem is the term $\hat{\mu}_\xi(t)$. The theorem states that the expected number of instances of any schema at the next time-step is directly proportional to its *observed* fitness (in the *current* population) relative to everything else in the population (subject to the effects of disruption, discussed in section 7). Thus, the ability of the schema theorem, which governs the behaviour of a simple genetic algorithm, to lead the search to interesting areas of the space is governed by the quality of the information it collects about the space through observed schema fitness averages in the population. It can be seen that if schemata tend to collect together solutions with related performance, then the fitness-variance of schemata will be relatively low, and the information that the schema theorem utilises will have predictive power for previously untested instances of schemata that the algorithm may generate. Conversely, if the schemata do not tend to collect together solutions with related performance, while the predictions the theorem makes about schema membership of the next population will continue to be accurate, the performance of the solutions that it generates cannot be assumed to bear any relation to the fitnesses of the parents. This clearly shows that it is essential that domain-specific knowledge be used in constructing a genetic algorithm, through the choice of representation and operators, whether this be implicit or—as is advocated in the present paper—explicit. If no domain-specific knowledge is used in selecting an appropriate representation, the algorithm will have no opportunity to exceed the performance of an enumerative search.

In addition to these observations about the schema theorem's representation-independence and the sensitivity of its predictions to the fitness variance of schemata, Vose (1991) and Radcliffe (1990) have independently proved that the "schema" theorem actually applies to *any* subset ξ of the search space, not only schemata, provided that the disruption coefficients $p_\omega p_\omega^\xi$ are computed appropriately for whichever set ξ is actually considered. Vose's response to this was to term a generalised schema a *predicate* and to investigate transformations of operators and representations that change problems that are hard for genetic algorithms into problems that are easy for them (Vose & Liepins, 1991b). This was achieved through exploiting a limited duality between operators and representations, which is discussed briefly in section 7. Radcliffe instead termed the generalised schemata *formae* (with singular form *forma*) and set out to develop a formalism to allow operators and representations to be developed with regard to stated assumptions about performance correlations in the search space. The aim was to maximise the predictive power of the Schema Theorem (and thus its ability to guide the search effectively) by allowing the developer of a genetic algorithm for some particular problem to codify knowledge about the search space by specifying families of formae that might reasonably be assumed to group together solutions with related performance.

The goal, then, of the present work, is to provide a mechanism for developing genetic representations and operators that allows the accuracy of the performance estimators $\hat{\mu}_\xi(t)$ to be maximised (or at least raised) by selecting appropriate subsets ξ. Knowledge about the search space is codified explicitly through constructing *equivalence relations* (q.v. section 3) that partition the search space into appropriate equivalence classes which play the rôle of formae. Having achieved this, the task addressed is the construction of a genetic representation and operators for searching the given space effectively.

3 Background on Equivalence Relations

Radcliffe (1990,1992b) has shown that domain specific knowledge must be utilised if a genetic algorithm is to have any opportunity to exceed the performance of an enumerative search. In schema analysis, this knowledge is used implicitly in the construction of an appropriate genetic representation. The way in which forma analysis captures and expresses this knowledge is through the introduction of *equivalence relations* over the search space $\mathcal{S}$. A relation is a property of each pair of members of $\mathcal{S}$ which is either true or false. Familiar examples are inequalities such as "greater than", defined over the integers. (For each pair of integers m and n, it is either true or false that $m > n$.) A relation $\sim$ is said to be an *equivalence relation* if it is reflexive, symmetric and transitive, and members for which such an equivalence relation is true are said to be *equivalent* under $\sim$. A relation is reflexive if and only if every member of $\mathcal{S}$ is equivalent to itself:f

$$\forall x \in \mathcal{S} : \; x \sim x. \tag{2}$$

Symmetry means that if one member of $\mathcal{S}$ is equivalent to another then the converse is true also:

$$\forall x, y \in \mathcal{S} : \; x \sim y \Longrightarrow y \sim x. \tag{3}$$

Transitivity requires that if a first member is equivalent to a second and that second is equivalent to a third then the first is equivalent to the third:

$$\forall x, y, z \in \mathcal{S} : \; (x \sim y \text{ and } y \sim z) \Longrightarrow x \sim z. \tag{4}$$

The most familiar equivalence relation is equality. For example, if the search space $\mathcal{S}$ is the set $\mathbb{Z}$ of integers, it is clearly true that

$$\begin{aligned} \forall x \in \mathbb{Z} : \quad & x = x, \\ \forall x, y \in \mathbb{Z} : \quad & x = y \Longrightarrow y = x, \\ \forall x, y, z \in \mathbb{Z} : \quad & (x = y \text{ and } y = z) \Longrightarrow x = z. \end{aligned} \tag{5}$$

It is easy to show that equivalence relations over $\mathcal{S}$ are equivalent to partitionings of $\mathcal{S}$ because they partition the search space into disjoint *equivalence classes* (figure 1), within which all the solutions are equivalent under the given equivalence relation.

In the context of genetic algorithms, certain equivalence relations will play the rôle of *genes* and certain equivalence classes will play the rôle of *alleles*. The idea will be to select equivalence relations that capture properties that are thought to be relevant to performance through appropriate equivalence relations and then to build operators that manipulate these properties in certain well-defined ways which will be described in later sections.

For example, if the search space were the space of all human beings, and the search were for the vainest person, it might be that eye colour would be thought to be an important determinant of performance (vanity). Eye colour is an equivalence relation because it plainly satisfies the conditions of reflexivity, symmetry and transitivity. (I have the same eye colour as myself; if I have the same eye colour as you, you must have the same eye colour as I; and if I have the same eye colour as you and you have the same eye colour as your friend, I too must have

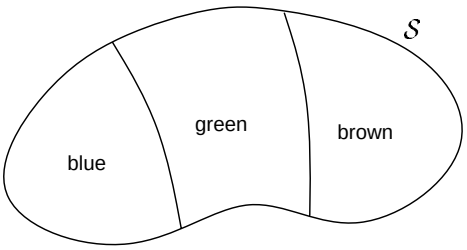

Figure 1: The eye colour equivalence relation partitions the search space $\mathcal{S}$ into disjoint equivalence classes corresponding to the various possible eye colours.

the same eye colour as she.) The equivalence classes are the sets of people with the various eye colours—blue-eyed people, brown-eyed people, green-eyed people and so forth. In this example, it is easy to see the natural association of the equivalence relation (eye colour) with the gene, and the equivalence class (blue eyes) with the allele.

Not all the equivalence relations will form genes: some will be composite. For example, if hair type is also introduced, it is quite proper to consider a combined equivalence relation which makes two people equivalent only if they share both hair type and eye colour. Indeed, such an equivalence relation will formally be constructed as the *intersection* of the more basic eye-colour and hair-type equivalence relations. It is only the simplest (non-composite) equivalence relations which will form genes.

For present purposes, it will be convenient to use a functional rather than a relational notation for equivalence relations. The follow definitions allow this.

Definition 1 ($\mathbb{B}$) Let $\mathbb{B} \triangleq \{0, 1\}$ so that $\mathbb{B}^n$ is the set of binary strings of length n. $\mathbb{B}$ will sometimes be interpreted as the set of truth values, with 0 corresponding to "false" and 1 to "true", sometimes as a set of numbers, and sometimes as a canonical two-element set.

■

Definition 2 (Equivalence relation) A function

$$\psi : \mathcal{S} \times \mathcal{S} \longrightarrow \mathbb{B} \tag{6}$$

will be said to be an *equivalence relation over* $\mathcal{S}$ if and only if

$$\begin{aligned} \forall x \in \mathcal{S} : \quad & \psi(x, x) = 1, \\ \forall x, y \in \mathcal{S} : \quad & \psi(x, y) = 1 \Longrightarrow \psi(y, x) = 1, \\ \text{and } \forall x, y, z \in \mathcal{S} : \quad & \psi(x, y) = \psi(y, z) = 1 \Longrightarrow \psi(x, z) = 1. \end{aligned} \tag{7}$$

■

Definition 3 (Identity Equivalence Relation $\mathcal{I}$) The *identity equivalence relation*

$$\mathcal{I} : \mathcal{S} \times \mathcal{S} \longrightarrow \mathbb{B} \tag{8}$$

is defined by

$$\mathcal{I}(x, y) \triangleq 1. \tag{9}$$

Plainly $\mathcal{I}$ is reflexive, symmetric and transitive.

■

Definition 4 ($\mathbb{E}$) Given a set $\mathcal{S}$, define $\mathbb{E}(\mathcal{S})$ to be the set of all equivalence relations over $\mathcal{S}$.

■

Equivalence classes will be seen to play an important rôle in the ensuing analysis. For convenience, the term *forma* (with plural *formae*) will be used to refer to an equivalence class. There will be three collections of formae that will be of particular interest. These are given below.

Definition 5 (Ξ) Given an equivalence relation $\psi \in \mathbb{E}(\mathcal{S})$, define Ξ_ψ to be the set of formae (equivalence classes) induced by ψ. Further, given a set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$, with $\Psi = \{\psi_1, \psi_2, \ldots, \psi_{|\Psi|}\}$, define Ξ_Ψ to be the vectors of formae given formally by

$$\Xi_\Psi \triangleq \prod_{i=1}^{|\Psi|} \Xi_{\psi_i} \equiv \Xi_{\psi_1} \times \Xi_{\psi_2} \times \cdots \times \Xi_{\psi_{|\Psi|}} \tag{10}$$

where the enumeration of the members of Ψ is understood to be arbitrary but fixed. Finally, $\Xi(\Psi)$ will be used to denote the set of all formae induced by relations in Ψ:

$$\Xi(\Psi) \triangleq \bigcup_{\psi \in \Psi} \Xi_\psi \equiv \Xi_{\psi_1} \cup \Xi_{\psi_2} \cup \cdots \cup \Xi_{\psi_{|\Psi|}}. \tag{11}$$

Ξ will also often be used to denote some general or specific set of formae.

■

Example 6 (Formae) Let ψ_e be the equivalence relation for eye colour, and assume for simplicity that the only three eye colours are green, brown and blue. Then

$$\Xi_{\psi_e} = \{\xi_{\text{green}}, \xi_{\text{brown}}, \xi_{\text{blue}}\}, \tag{12}$$

where ξ_{green}, for example, is the forma containing all members of $\mathcal{S}$ with green eyes. Similarly, let ψ_h be the equivalence relation for hair type, with formae corresponding to straight and curly hair, so that

$$\Xi_{\psi_h} = \{\xi_{\text{curly}}, \xi_{\text{straight}}\}. \tag{13}$$

Now let

$$E = \{\psi_e, \psi_h\}. \tag{14}$$

Then

$$\begin{aligned}
\Xi_E &= \Xi_{\psi_e} \times \Xi_{\psi_h} && (15)\\
&= \{\xi_{\text{green}}, \xi_{\text{brown}}, \xi_{\text{blue}}\} \times \{\xi_{\text{curly}}, \xi_{\text{straight}}\} && (16)\\
&= \{(\xi_{\text{green}}, \xi_{\text{curly}}), \quad (\xi_{\text{brown}}, \xi_{\text{curly}}), \quad (\xi_{\text{blue}}, \xi_{\text{curly}}),\\
&\quad (\xi_{\text{green}}, \xi_{\text{straight}}), \quad (\xi_{\text{brown}}, \xi_{\text{straight}}), \quad (\xi_{\text{blue}}, \xi_{\text{straight}})\}
\end{aligned}$$

and

$$\Xi(E) = \{\xi_{\text{green}}, \xi_{\text{brown}}, \xi_{\text{blue}}, \xi_{\text{curly}}, \xi_{\text{straight}}\}. \tag{17}$$

■

4 The Algebra of Equivalence Relations

In order to formalise the notions of gene, allele and so forth in terms of equivalence relations, notions from linear algebra are borrowed and modified as appropriate. In what follows, intersection of equivalence relations is introduced and is used as the analogue of linear combination in linear algebra. This allows the *span* of a set of equivalence relations to be defined as the set of all equivalence relations that can be constructed by their intersection. It further allows notions of independence and orthogonality to be established. These suffice to allow the introduction of both orthogonal and non-orthogonal bases, which—as will be seen—are fundamentally related to genes and alleles. In the following section (section 5) these will be used to construct genetic operators and to analyse their properties.

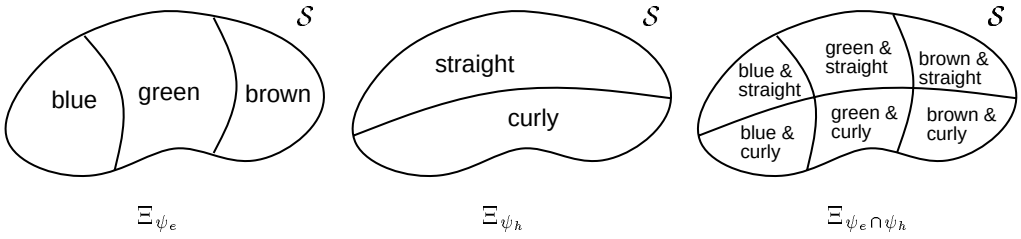

Figure 2: The intersection of a pair of equivalence relations is defined to be their logical conjunction.

Definition 7 (Intersection of equivalence relations) Given equivalence relations $\psi, \phi \in \mathbb{E}(\mathcal{S})$, define their intersection

$$\psi \cap \phi : \mathcal{S} \times \mathcal{S} \longrightarrow \mathbb{B} \tag{18}$$

by

$$(\psi \cap \phi)(x, y) \triangleq \psi(x, y) \wedge \phi(x, y) \tag{19}$$

where $\wedge$ denotes logical conjunction ("and") defined by

$$a \wedge b \triangleq \begin{cases} 1, & \text{if } a = b = 1, \\ 0, & \text{otherwise.} \end{cases} \tag{20}$$

■

Two solutions are thus equivalent under the intersection of a pair of equivalence relations precisely if they are equivalent under each of the pair. Intersection is illustrated in figure 2.

It is trivial to show that the intersection of two equivalence relations so defined is itself an equivalence relation. It is also easy to see that this definition of intersection is commutative and associative, since these properties follow from the commutativity and associativity of logical conjunction. Thus given a set Ψ of equivalence relations, the intersection of any $A \subset \Psi$ is well defined and will be denoted $\cap A$. If

$$A = \{\psi_1, \psi_2, \ldots, \psi_{|A|}\} \tag{21}$$

then

$$\bigcap A \triangleq \bigcap_{\psi \in A} \psi \equiv \psi_1 \cap \psi_2 \cap \cdots \cap \psi_{|A|}. \tag{22}$$

The formae (equivalence classes) induced by $\psi \cap \phi$ are intersections of the formae induced by ψ and ϕ, as the following lemma shows.

Lemma 8 (Formae induced by intersections are intersections of formae) *Given a set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$, let $\phi \triangleq \cap\Psi$. Then the equivalence classes (formae) induced by ϕ are intersections of those induced by the relations in Ψ. Formally*

$$\forall \xi \in \Xi_\phi \; \exists \boldsymbol{\xi} \in \Xi_\Psi : \bigcap_{i=1}^{|\Psi|} \xi_i = \xi, \tag{23}$$

where $\boldsymbol{\xi} = (\xi_1, \xi_2, \ldots, \xi_{|\Psi|})$.

Proof: Given solutions x and y in $\mathcal{S}$, and any equivalence relation $\psi \in \mathbb{E}(\mathcal{S})$, let $[x]_\psi$ denote the equivalence class under ψ in which x lies (i.e. the set of all solutions that are equivalent to x under ψ). Then

$$\begin{aligned} \phi(x,y) = 1 \quad &\iff \quad y \in [x]_\phi && (24)\\ &\iff \quad \forall \psi \in \Psi : \ \psi(x,y) = 1 && (25)\\ &\iff \quad \forall \psi \in \Psi : \ y \in [x]_\psi = 1 && (26)\\ &\iff \quad y \in \bigcap \left\{ [x]_\psi \ \middle| \ \psi \in \Psi \right\}. && (27) \end{aligned}$$

Thus, comparing equations 24 and 27,

$$[x]_\phi = \bigcap \left\{ [x]_\psi \ \middle| \ \psi \in \Psi \right\}. \tag{28}$$

This is an intersection of precisely the form required by equation 23.

□

Definition 9 (Power Set) The *power set* of any set A is the set of all subsets of that set and is denoted $\mathbb{P}(A)$. Thus

$$\mathbb{P}(A) \triangleq \{B \subset A\}. \tag{29}$$

■

Definition 10 (Span) The *span* of a set of equivalence relations $E \subset \mathbb{E}(\mathcal{S})$ is defined to be the set of all equivalence relations that can be constructed by intersection of any subset of E. Formally,

$$\text{Span} \ : \mathbb{P}(\mathbb{E}(\mathcal{S})) \longrightarrow \mathbb{P}(\mathbb{E}(\mathcal{S})) \tag{30}$$

is defined by

$$\text{Span}\ E \triangleq \left\{ \varepsilon \in \mathbb{E}(\mathcal{S}) \ \middle| \ \exists\, A_\varepsilon \subset E : \bigcap A_\varepsilon = \varepsilon \right\}. \tag{31}$$

If $\Psi \subset \text{Span}\ E$ then E is said to *span* Ψ.

■

Example 11 (Span) Given an arbitrary pair of equivalence relations ψ_e and ψ_h, but thinking of them as the eye colour and hair type relations introduced in example 6 above,

$$\text{Span}\ \{\psi_e, \psi_h\} = \{\psi_e, \psi_h, \psi_{eh}\} \tag{32}$$

where

$$\psi_{eh} \triangleq \psi_e \cap \psi_h. \tag{33}$$

ψ_{eh} makes two solutions equivalent only if they share both eye colour and hair type.

■

Definition 12 (Independence) A set of equivalence relations $E \subset \mathbb{E}(\mathcal{S})$ is said to be *independent* if no member of E can be constructed by intersection of other members of E. Formally, E is independent if and only if

$$\forall \varepsilon \in E \ \nexists\, A_\varepsilon \subset E \setminus \{\varepsilon\} : \bigcap A_\varepsilon = \varepsilon, \tag{34}$$

where $\setminus$ denotes set subtraction.[1]

■

Example 13 (Independence) $\{\psi_e, \psi_h\}$ and $\{\psi_e, \psi_{eh}\}$, from example 11, are both independent sets of equivalence relations, but $\{\psi_e, \psi_h, \psi_{eh}\}$ is not because $\psi_{eh} = \psi_e \cap \psi_h$.

■

[1] Given sets A and B, $A \setminus B = \{a \in A \ \middle| \ a \notin B\}$.

Definition 14 (Orthogonality) A set of equivalence relations $E \subset \mathbb{E}(\mathcal{S})$ is said to be *orthogonal to order* k if given any k equivalence classes induced by different members of E, their intersection is non-empty. Formally, E is orthogonal to order k if and only if

$$\forall A \subset E \; (|A| \leq k) \; \forall \boldsymbol{\xi} \in \Xi_A : \bigcap_{i=1}^{|A|} \xi_i \neq \varnothing, \tag{35}$$

where $\boldsymbol{\xi} = (\xi_1, \xi_2, \ldots, \xi_{|A|})$. If E is orthogonal to order $|E|$ then E is simply said to be orthogonal,[2] in which case equation 35 simplifies to

$$\forall \boldsymbol{\xi} \in \Xi_E : \bigcap_{i=1}^{|E|} \xi_i \neq \varnothing. \tag{36}$$

■

Example 15 (Orthogonality) Assuming that all combinations of eye colour and hair type are possible (or, more carefully, that at least one instance of each combination exists in the search space $\mathcal{S}$ over which the equivalence relations are defined) the set $\{\psi_e, \psi_h\} \subset \mathbb{E}(\mathcal{S})$ is orthogonal, but $\{\psi_e, \psi_{eh}\} \subset \mathbb{E}(\mathcal{S})$ is not because, for example,

$$\xi_{\text{green}} \cap \xi_{\text{blue,curly}} = \varnothing, \tag{37}$$

contradicting equation 36. If it were impossible to have, say, green eyes and straight hair, then $\{\psi_e, \psi_h\}$ would also be non-orthogonal.

■

It is clear that orthogonality is a stronger condition than independence. The following lemma confirms, as might be expected from the analogy with linear algebra, that orthogonality implies independence. (The hurried reader could skip the proof of this lemma without imperiling future understanding.)

Lemma 16 (Orthogonality implies independence) *Let $\Psi \subset \mathbb{E}(\mathcal{S})$ be an orthogonal set of equivalence relations over $\mathcal{S}$. Then Ψ is independent.*

Proof: Suppose that Ψ were not independent. Then, from the definition of independence (equation 34), there would be some ψ in Ψ that could be constructed as the intersection of some other members of Ψ:

$$\exists \, \psi \in \Psi \; \exists \, A_\psi \subset \Psi \setminus \{\psi\} : \bigcap A_\psi = \psi. \tag{38}$$

For each member ϕ of A_ψ, choose an arbitrary equivalence class $\xi_\phi \in \Xi_\phi$. Then, by construction, the intersection

$$\xi \triangleq \bigcap \{\xi_\phi \mid \phi \in A_\psi\} \tag{39}$$

is an equivalence class induced by ψ (because $\psi = \bigcap A_\psi$). Thus any solution that is in each of the formae ξ_ϕ will fail to be in any equivalence class chosen for ψ except ξ since the formae induced by a single equivalence relation are disjoint (non-intersecting). Thus provided that $|\Xi_\psi| > 1$, which is true for all equivalence relations except the identity, a forma $\xi' \in \Xi_\psi \setminus \{\xi\}$ must exist such that

$$\varnothing = \xi \cap \xi' = \left(\bigcap \{\xi_\phi \mid \phi \in A_\phi\} \right) \cap \xi', \tag{40}$$

contradicting orthogonality (equation 36). Since it is obvious that the identity equivalence relation cannot be constructed by intersection of other equivalence relations, this concludes the proof.

□

Following the analogy with linear algebra, a basis can now be defined in the obvious way.

[2] In Radcliffe (1991b) orthogonality was defined to be what is here defined as orthogonality to order two (pair-wise orthogonality). This definition is unsatisfactory because pair-wise orthogonality does not imply full orthogonality in the sense of this exposition. This was not realised at the time the earlier definition was given. The earlier definition should be discarded in favour of that given in the present treatment.

Definition 17 (Basis) A subset E of a set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$ will be said to constitute a *basis* for Ψ if and only if E spans Ψ and E is independent. If E is orthogonal, the basis will be said to be an *orthogonal basis.* The number of elements in a basis E will be referred to as the *dimension* of the basis.

■

5 Representation

One of the uses for a basis in linear algebra is that it allows an arbitrary vector, defined as a geometric entity, to be "coordinatised" by projecting it onto the axes defined by the "basic vectors" which constitute the basis. The vector can then be described as a linear combination of the basic vectors. A similar process is now possible for the equivalence relations in Ψ if there is a basis E for Ψ: a general equivalence relation can be decomposed as an intersection of "basic equivalence relations" in E. This decomposition underpins the forthcoming formalisation of genes and alleles, and facilitates the expression of criteria against which genetic operators can be measured. It further provides a framework within which to discuss the amenability of various problems to genetic search.

The mechanism here adopted for formalising the notions of genes and alleles involves identifying Ξ_E as a representation of $\mathcal{S}$. In order for this to be useful, ideally Ξ_E should be isomorphic to $\mathcal{S}$ under a function induced by the basic equivalence relations as follows.

Definition 18 (ρ) Given an equivalence relation $\varepsilon \in \mathbb{E}(\mathcal{S})$, define the *partial representation function*

$$\rho_\varepsilon : \mathcal{S} \longrightarrow \Xi_\varepsilon \tag{41}$$

by

$$\rho_\varepsilon(x) \triangleq [x]_\varepsilon \tag{42}$$

where $[x]_\varepsilon$ is the equivalence class of x under ε:

$$[x]_\varepsilon \triangleq \left\{ y \in \mathcal{S} \;\middle|\; \varepsilon(x, y) = 1 \right\}. \tag{43}$$

Then, given any $E \subset \mathbb{E}(\mathcal{S})$, with $E = \{ \varepsilon_1, \varepsilon_2, \ldots, \varepsilon_n \}$, define the *genetic representation function* by

$$\boldsymbol{\rho}_E \triangleq (\rho_{\varepsilon_1}, \rho_{\varepsilon_2}, \ldots, \rho_{\varepsilon_n}) \tag{44}$$

so that

$$\boldsymbol{\rho}_E : \mathcal{S} \longrightarrow \Xi_E \tag{45}$$

with

$$\boldsymbol{\rho}_E(x) = ([x]_{\varepsilon_1}, [x]_{\varepsilon_2}, \ldots, [x]_{\varepsilon_n}). \tag{46}$$

■

The function $\boldsymbol{\rho}_E$ maps each solution in $\mathcal{S}$ to the vector of basic formae to which it belongs, and can be used as a representation of $\mathcal{S}$ as follows.

Definition 19 ($\mathcal{C}$) Given a basis E for a set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$, define $\mathcal{C}$, the space of *chromosomes,* to be the image of $\mathcal{S}$ under $\boldsymbol{\rho}_E$:

$$\mathcal{C} \triangleq \operatorname*{Im}_{\boldsymbol{\rho}_E} \mathcal{S} \equiv \boldsymbol{\rho}_E(\mathcal{S}) \equiv \left\{ \boldsymbol{\xi} \in \Xi_E \;\middle|\; \exists\, x \in \mathcal{S} :\ \boldsymbol{\rho}_E(x) = \boldsymbol{\xi} \right\} \subset \Xi_E. \tag{47}$$

■

Observation 20 Provided that ρ_E is injective (i.e., different solutions have different representations in $\mathcal{C}$) the growth function

$$g : \mathcal{C} \longrightarrow \mathcal{S}, \tag{48}$$

which produces the corresponding solution in $\mathcal{S}$ given its chromosomal representative ξ, is simply the inverse of ρ_E:

$$g(\xi) \triangleq \rho_E^{-1}(\xi). \tag{49}$$

The necessity for injectivity so that the inverse is well defined is brought out in the definition of coverage which follows.

■

The remainder of this section clarifies the relationship between representations and orthogonality, and shows that a unique basis can always be found for an arbitrary set of equivalence relations over the search space. While earlier discussions of forma analysis have advocated non-redundant representations, they have never explicitly imposed the covering condition about to be introduced, or discussed the representation function in quite this manner.

First, the notion of *coverage* is introduced. The idea here is that for a set of equivalence relations to induce a useful genetic representation, it must be sufficiently rich that a solution can be uniquely identified by examining the equivalence classes to which it belongs. After a couple of technical lemmas, it is then shown that an orthogonal basis that satisfies such a requirement of coverage may be used to generate a faithful representation of the search space automatically. After another technical lemma, it is shown that, in contrast to the analogous case in linear algebra, the basis for any set of equivalence relations is unique. Combined with the previous result, this means that any sufficiently rich set of equivalence relations over the search space induces a unique genetic representation. At this point, genes and alleles are formally identified as basic equivalence relations and basic formae respectively. Finally, the twin notions of a *similarity set* and a *dynastic potential* are introduced. These group together related solutions in ways that are potentially relevant to recombination, which is then discussed in section 6. The impatient reader is again recommended to skip the proofs of the lemmas in the remainder of this section.

Definition 21 (Coverage) A set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$ will be said to *cover* $\mathcal{S}$ if and only if for each pair of solutions in $\mathcal{S}$ there is at least one equivalence relation in Ψ under which the pair are not equivalent. Formally,

$$\forall x \in \mathcal{S}\, \forall y \in \mathcal{S} \setminus \{x\}\, \exists\, \psi \in \Psi :\ \psi(x, y) = 0. \tag{50}$$

■

Lemma 22 (A basis for a covering set covers) *Let E be a basis for a set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$ that covers $\mathcal{S}$. Then E covers $\mathcal{S}$.*

Proof: This follows immediately since every equivalence relation ψ in Ψ can be expressed as an intersection of some members of the basis E, and thus if ψ distinguishes between two solutions so must at least one of the equivalence relations in E into which it can be decomposed.

□

Coverage is important because if a set of equivalence relations covers $\mathcal{S}$ then specifying to which equivalence class a solution belongs for each of the equivalence relations in the set suffices to identify a solution uniquely. This is clearly an important property of any genetic representation.

Observation 23 A rather pleasing alternative to the definition of coverage given above introduces the *fundamental equivalence relation*

$$\chi \triangleq \bigcap \Psi. \tag{51}$$

Coverage is then easily seen to reduce to the requirement that under χ, each member of $\mathcal{S}$ is equivalent only to itself. Formally, Ψ covers $\mathcal{S}$ if and only if

$$\chi(x, y) \equiv \delta_{xy}, \tag{52}$$

where δ is the "Kronecker Delta", defined by

$$\delta_{ij} \triangleq \begin{cases} 1, & \text{if } i = j, \\ 0, & \text{otherwise,} \end{cases} \tag{53}$$

so that each solution is in a singleton equivalence class under χ:

$$\rho_\chi(x) \equiv [x]_\chi \equiv \{x\}. \tag{54}$$

■

Lemma 24 *A basis E for a set Ψ of equivalence relations over $\mathcal{S}$ is orthogonal if and only if the genetic representation function $\boldsymbol{\rho}_E : \mathcal{S} \longrightarrow \Xi_E$ is surjective, i.e. if $\boldsymbol{\rho}_E(\mathcal{S}) = \Xi_E$.*

Proof: Recall from the definition of $\boldsymbol{\rho}_E$ in equations 45 and 46 that

$$\boldsymbol{\rho}_E : \mathcal{S} \longrightarrow \Xi_E \tag{45 bis}$$

is given by

$$\boldsymbol{\rho}_E(x) = ([x]_{\varepsilon_1}, [x]_{\varepsilon_2}, \ldots, [x]_{\varepsilon_{|E|}}) \tag{46 bis}$$

where $E = \{\varepsilon_1, \varepsilon_2, \ldots, \varepsilon_{|E|}\}$. Thus if $\boldsymbol{\rho}_E$ is surjective, this means that

$$\boldsymbol{\rho}_E(\mathcal{S}) = \Xi_E \tag{55}$$

$$\iff \quad \forall \boldsymbol{\xi} \in \Xi_E \; \exists\, x \in \mathcal{S} : \boldsymbol{\rho}_E(x) = \boldsymbol{\xi} \tag{56}$$

$$\iff \quad \forall \boldsymbol{\xi} \in \Xi_E \; \exists\, x \in \mathcal{S} : x \in \bigcap_{i=1}^{|E|} \xi_i \tag{57}$$

$$\iff \quad \forall \boldsymbol{\xi} \in \Xi_E : \bigcap_{i=1}^{|E|} \xi_i \neq \varnothing, \tag{58}$$

where, as usual, $\boldsymbol{\xi} = (\xi_1, \xi_2, \ldots, \xi_{|E|})$. Since this is precisely the orthogonality condition given in equation 36, this concludes the proof. □

Theorem 25 (An orthogonal covering basis induces a faithful representation) *Let E be an orthogonal basis for a set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$ that covers $\mathcal{S}$. Then Ξ_E is a faithful representation of $\mathcal{S}$ (i.e. $\boldsymbol{\rho}_E$ is invertible).*

Proof: Lemma 24 has shown that $\boldsymbol{\rho}_E$ is surjective whenever E is orthogonal, so it only remains to be shown that if Ψ covers $\mathcal{S}$ then $\boldsymbol{\rho}_E$ is injective. Moreover, lemma 22 shows that it suffices to demonstrate that if E covers $\mathcal{S}$ then $\boldsymbol{\rho}_E$ is injective. But this is obvious, because for a basis to cover $\mathcal{S}$ means precisely that for each pair of solutions, (at least) one of the basic equivalence relations distinguishes between them, and thus they must lie in different basic formae for that equivalence relation. Since the representation furnished by $\boldsymbol{\rho}_E$ is precisely the vector of basic formae to which a solution belongs, it follows that if E covers $\mathcal{S}$, this function must be injective as required.

□

It would be convenient if every set of equivalence relations were known to contain a basis, and even more convenient if that basis were always unique. The following definition and lemma facilitate the proof of theorem 29, which shows that this is so. Again, the proof of the lemma is merely technical, and may be safely skipped by the hurried reader.

Definition 26 (Precision) The *precision* of an equivalence relation ψ is the number of equivalence classes it induces,[3] and is denoted $p(\psi)$.

■

Remark 27 Plainly any equivalence relation except the identity $\mathcal{I}$ has precision greater than 1.

■

Lemma 28 (Precision of Intersections) *Given equivalence relations $\psi, \phi \in \mathbb{E}(\mathcal{S})$, with $\psi \neq \psi \cap \phi \neq \phi$, the number of equivalence classes induced by $\psi \cap \phi$ exceeds the number induced by either ψ or ϕ, i.e.*

$$p(\psi \cap \phi) > \max\{p(\psi), p(\phi)\}. \tag{59}$$

Proof: Without loss of generality, assume that $p(\psi) \geq p(\phi)$. From the definition of intersection of equivalence relations (equation 19), it is clear that solutions that lie in different equivalence classes under ψ must also lie in different equivalence classes under $\psi \cap \phi$, so $p(\psi \cap \phi) \geq p(\psi)$. Since $\psi \neq \psi \cap \phi$ by assumption, it is also clear that some pair of solutions that are in the same equivalence class under ψ must be in different equivalence classes under $\psi \cap \phi$, otherwise ψ and $\psi \cap \phi$ would be identical. Since equivalence classes are disjoint, this means that at least one of the equivalence classes of ψ must be divided in $\psi \cap \phi$, and thus at least one more equivalence class must be induced by $\psi \cap \phi$ than by ψ, as asserted.

□

Theorem 29 (Existence of unique basis) *Every set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$ contains a unique basis.*

Proof: Existence (by construction):

A basis E can be constructed using the following recursive definitions.

1. Let $N \triangleq |\Psi|$ and arbitrarily enumerate the members of Ψ as $\psi_1, \psi_2, \ldots, \psi_N$.
2. Let $E_0 \triangleq \Psi$.
3. Recursively define E_k (for $k \leq N$) by

$$E_k \triangleq \begin{cases} E_{k-1} \setminus \{\psi_k\}, & \text{if } \exists\, A \subset E_{k-1} \setminus \{\psi_k\} : \bigcap A = \psi_k, \\ E_{k-1}, & \text{otherwise.} \end{cases} \tag{60}$$

4. Let $E \triangleq E_N$.

The set E thus constructed is clearly independent, because any member that could be constructed by intersecting others has been explicitly removed. Moreover, it is clear that E_k spans E_{k-1} by construction, and that spanning is transitive, so that $E = E_N$ must span $E_0 = \Psi$. Thus E is indeed a basis for Ψ.

Uniqueness:

Suppose that E_1 and E_2 are both bases for Ψ, with $E_1 \neq E_2$. Then there must be some relation ε that is in E_1 but not E_2:

$$\exists\, \varepsilon \in E_1 \cap E_2' \tag{61}$$

where the prime denotes complementation:

$$E_2' \triangleq \mathbb{E}(\mathcal{S}) \setminus E_2. \tag{62}$$

[3] In previous discussions, the precision of a forma was defined as the precision of the equivalence relation that induces it, but this is clearly only well-defined if the forma is induced by only one equivalence relation. There is therefore no attempt to define the precision of a forma in this paper.

Since E_2 is a basis for Ψ, however,

$$\exists\, A_\varepsilon \subset E_2 : \bigcap A_\varepsilon = \varepsilon. \tag{63}$$

Assume, without loss of generality, that A_ε is the smallest such set, so that no subset of A_ε suffices to make up ε. Since $\varepsilon \notin E_2$, if follows that $|A_\varepsilon| > 1$.

Now, since E_1 is a basis for Ψ, each $\phi \in A_\varepsilon$ can be constructed as an intersection of relations in E_1:

$$\forall \phi \in A_\varepsilon\ \exists\, A_\phi \subset E_1 : \bigcap A_\phi = \phi. \tag{64}$$

Let B_ε be that subset of the relations in E_1 used to make up any of the relations ϕ from $A_\varepsilon \subset E_2$ whose intersection forms ε:

$$B_\varepsilon \triangleq \bigcup \left\{ A_\phi \;\middle|\; \phi \in A_\varepsilon \right\} \subset E_1. \tag{65}$$

Clearly

$$\bigcap B_\varepsilon = \varepsilon, \tag{66}$$

so by independence of E_1, B_ε must contain ε. Since $\varepsilon \notin E_2$ and $A_\varepsilon \subset E_2$, some $\phi \in A_\varepsilon$ must be the intersection of ε with some other relation or relations in B_ε. By lemma 28, $p(\phi) > p(\varepsilon)$. But by the same lemma, this prevents ϕ being used in the construction of ε as an intersection of the members of A_ε. This is a contradiction, so a basis for Ψ is indeed unique.

□

This theorem shows that every set of equivalence relations uniquely specifies a genetic representation function. It is thus now appropriate to define genes and alleles.

Definition 30 (Genes and Alleles) Let E be a basis for a set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$ that covers $\mathcal{S}$. The members of E will be called *basic equivalence relations,* or *genes.* Similarly, given any $\varepsilon \in E$, the members of Ξ_ε will be called *basic formae,* or *alleles.*

■

Definition 31 (Dynastic Potential) Given the basis E for a set $\Psi \subset \mathbb{E}(\mathcal{S})$ of equivalence relations that covers a search space $\mathcal{S}$, the *dynastic potential*

$$\Gamma : \mathbb{P}(\mathcal{S}) \longrightarrow \mathbb{P}(\mathcal{S}) \tag{67}$$

of a subset L of $\mathcal{S}$ is the set of all solutions in $\mathcal{S}$ that are equivalent to at least one of the members of L under each of the basic equivalence relations (genes) in E:

$$\Gamma(L) \triangleq \left\{ z \in \mathcal{S} \;\middle|\; \forall \varepsilon \in E\ \exists\, x \in L :\ \varepsilon(x, z) = 1 \right\}. \tag{68}$$

This is the set of all "children" that can be generated using only alleles available from the "parent" solutions in L.

■

Definition 32 (Similarity Set) Let Ξ be a set of formae defined over a search space $\mathcal{S}$. Then the *similarity set* of any $L \subset \mathcal{S}$ (defined with respect to Ξ and written $\Sigma(L)$) is the intersection of all those formae to which each solution in L belongs:

$$\Sigma(L) \triangleq \begin{cases} \bigcap \{ \xi \in \Xi \;\middle|\; L \subset \xi \}, & \text{if } \exists\, \xi \in \Xi :\ L \subset \xi, \\ \mathcal{S}, & \text{otherwise.} \end{cases} \tag{69}$$

■

Remark 33 It is usually (but not invariably) the case that formae satisfy a closure condition provided that they are augmented by the empty set, so that the intersection of any pair of formae is itself a forma. If this is the case, it is clear that the similarity set of a set L of solutions is simply the smallest forma that contains L.

■

Example 34 (Dynastic Potential and Similarity Set) Let E be an orthogonal basis for a set Ψ of equivalence relations that covers a search space $\mathcal{S}$. Let

$$E = \{\varepsilon_e, \varepsilon_h, \varepsilon_p\}, \tag{70}$$

these being equivalence relations for eye colour, hair type and political persuasion, with equivalence classes given by

$$\Xi_{\varepsilon_e} = \{\xi_{\text{blue}}, \xi_{\text{green}}, \xi_{\text{brown}}\}, \tag{71}$$

$$\Xi_{\varepsilon_h} = \{\xi_{\text{straight}}, \xi_{\text{curly}}\}, \tag{72}$$

$$\Xi_{\varepsilon_p} = \{\xi_{\text{left}}, \xi_{\text{right}}\}. \tag{73}$$

Orthogonality means that all combinations of gene values are legal, so the search space has $3 \times 2 \times 2 = 12$ members. Now consider two solutions x and y with genetic representations given by

$$\boldsymbol{\rho}_E(x) = (\xi_{\text{blue}}, \xi_{\text{straight}}, \xi_{\text{left}}) \tag{74}$$

and

$$\boldsymbol{\rho}_E(y) = (\xi_{\text{green}}, \xi_{\text{curly}}, \xi_{\text{left}}). \tag{75}$$

Then the dynastic potential $\Gamma(\{x, y\})$ is given by

$$\Gamma(\{x, y\}) = (\xi_{\text{blue}} \cup \xi_{\text{green}}) \cap (\xi_{\text{straight}} \cup \xi_{\text{curly}}) \cap \xi_{\text{left}} \tag{76}$$

$$\begin{aligned} \iff \boldsymbol{\rho}_E(\Gamma(\{x, y\})) = \big\{ & (\xi_{\text{blue}}, \xi_{\text{straight}}, \xi_{\text{left}}), \quad (\xi_{\text{green}}, \xi_{\text{straight}}, \xi_{\text{left}}), \\ & (\xi_{\text{blue}}, \xi_{\text{curly}}, \xi_{\text{left}}), \quad (\xi_{\text{green}}, \xi_{\text{curly}}\xi_{\text{left}}) \quad \big\} \end{aligned} \tag{77}$$

while the similarity set $\Sigma(\{x, y\})$ is given by

$$\Sigma(\{x, y\}) = \xi_{\text{left}} \tag{78}$$

$$\begin{aligned} \iff \boldsymbol{\rho}_E(\Sigma(\{x, y\})) = \big\{ & (\xi_{\text{blue}}, \xi_{\text{straight}}, \xi_{\text{left}}), \quad (\xi_{\text{blue}}, \xi_{\text{curly}}, \xi_{\text{left}}), \\ & (\xi_{\text{green}}, \xi_{\text{straight}}, \xi_{\text{left}}), \quad (\xi_{\text{green}}, \xi_{\text{curly}}, \xi_{\text{left}}), \\ & (\xi_{\text{brown}}, \xi_{\text{straight}}, \xi_{\text{left}}), \quad (\xi_{\text{brown}}, \xi_{\text{curly}}, \xi_{\text{left}}) \big\} \end{aligned} \tag{79}$$

Thus the similarity set of a pair of parents contains all those solutions that share the same alleles as the parents share, whereas the dynastic potential is restricted to those that have every allele in common with one or other parent.

■

Lemma 35 (Similarity sets contain dynastic potentials) *Given a basis E for a set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$, the dynastic potential of any subset L of $\mathcal{S}$ is contained by the similarity set of L. Formally,*

$$\forall L \subset \mathcal{S} : \ \Gamma(L) \subset \Sigma(L). \tag{80}$$

Proof: Recall from definition 32 that the similarity set of a set L of solutions is given by

$$\Sigma(L) \triangleq \begin{cases} \bigcap \{\xi \in \Xi \mid L \subset \xi\}, & \text{if } \exists \xi \in \Xi : \ L \subset \xi, \\ \mathcal{S}, & \text{otherwise,} \end{cases} \tag{69 bis}$$

while from definition 31, their dynastic potential is

$$\Gamma(L) \triangleq \left\{ z \in \mathcal{S} \mid \forall \varepsilon \in E \ \exists x \in L : \ \varepsilon(x, z) = 1 \right\}. \tag{68 bis}$$

Clearly if $\Sigma(L) = \mathcal{S}$ the result is trivial, so it remains only to deal with the case in which

$$\Sigma(L) = \bigcap \{\xi \in \Xi \mid L \subset \xi\}. \tag{81}$$

Let $\Psi_L^\star$ denote the subset of the equivalence relations in Ψ under which all the members of L are equivalent. Similarly, let $E_L^\star$ denote the subset of the basic equivalence relations in E under which all the members of L are equivalent. Then equation 81 may be re-expressed as

$$\Sigma(L) = \{z \in \mathcal{S} \mid \forall \psi \in \Psi_L^\star \; \exists \, x \in L : \; \psi(x, z) = 1\}. \tag{82}$$

But because E is a basis for Ψ, equation 82 must remain true if $\Psi_L^\star$ is replaced with $E_L^\star$ as follows:

$$\Sigma(L) = \{z \in \mathcal{S} \mid \forall \varepsilon \in E_L^\star \; \exists \, x \in L : \; \varepsilon(x, z) = 1\}. \tag{83}$$

Expressed in this form, it becomes clear that the dynastic potential specified in equation 68 (bis) is merely a restriction of the similarity set (since $E_L^\star \subset E$). This completes the proof. □

6 Recombination

Having introduced the formalism of equivalence relations and constructed an algebra that naturally leads to the identification of genes and alleles, it is now appropriate to consider how recombination operators should be constructed so as to manipulate these structures in useful ways. It will be convenient to regard a recombination operator as any function that, given some pair of solutions together with some "control parameter", produces a unique child. (In the case of one-point crossover, for example, the control parameter is the cross point.) This formalism allows the stochastic element in recombination to be introduced simply through the choice of control parameter. It will normally be assumed that the control parameter is selected from a uniform distribution over the control set, though other distributions could be used. After some basic definitions, various properties that might be thought to characterise good recombination operators will be introduced.

Definition 36 (Recombination) Given any (non-empty) set $\mathcal{K}_X$, and a search space $\mathcal{S}$, any function

$$X : \mathcal{S} \times \mathcal{S} \times \mathcal{K}_X \longrightarrow \mathcal{S} \tag{84}$$

will be said to be a *recombination operator over* $\mathcal{S}$, and the set $\mathcal{K}_X$ will be called the *control set* for X.
■

Definition 37 (Dynastic Span) Let X be a recombination operator over a search space $\mathcal{S}$ with control set $\mathcal{K}_X$. Then the *immediate dynastic span* (under X)

$$\Gamma_X^1 : \mathbb{P}(\mathcal{S}) \longrightarrow \mathbb{P}(\mathcal{S}) \tag{85}$$

of a set $L \subset \mathcal{S}$ of solutions is the set of all children that can be produced by recombining the members of L with any control parameter:

$$\Gamma_X^1(L) \triangleq \{z \in \mathcal{S} \mid \exists \, x, y \in L \; \exists \, k \in \mathcal{K}_X : \; X(x, y, k) = z\}. \tag{86}$$

The *ith dynastic span* (under X)

$$\Gamma_X^i : \mathbb{P}(\mathcal{S}) \longrightarrow \mathbb{P}(\mathcal{S}) \tag{87}$$

is then defined recursively as follows:

$$\Gamma_X^i(L) \triangleq \Gamma_X^1(\Gamma_X^{i-1}(L)). \tag{88}$$

Thus $\Gamma_X^i(L)$ is the set of children that can be produced by i recombinations of previous generations. Finally, the (full) *dynastic span* (under X),

$$\Gamma_X : \mathbb{P}(\mathcal{S}) \longrightarrow \mathbb{P}(\mathcal{S}) \tag{89}$$

of a set $L \subset \mathcal{S}$ is the set of all children that can be produced given any number of generations, so that

$$\Gamma_X(L) \triangleq \bigcup_{i=1}^{\infty} \Gamma_X^i(L). \tag{90}$$

■

The definitions of recombination operators, dynastic spans and dynastic potentials used in this paper are convenient, and allow distinctions to be drawn between operators which, while having the same dynastic span, produce children with different probabilities or frequencies. This can be accommodated by using different control sets, possibly having a number of control parameters each of which results in the production of the same child. While the different "distributional" characteristics of operators can be highly significant, the focus of the following definitions will be only the dynastic span of an operator for various pairs of parents. It will therefore be convenient to introduce an equivalence relation $\sim$ on recombination operators that makes them equivalent precisely if they have the same dynastic span for each subset of $\mathcal{S}$. The following definition achieves this.

Definition 38 (Dynastic Equivalence) Two recombination operators X_1 and X_2, each defined over a search space $\mathcal{S}$, and having respective control sets $\mathcal{K}_{X_1}$ and $\mathcal{K}_{X_2}$, will be said to be *dynastically equivalent* if and only if the range of (first generation) children each is capable of producing given any set of parents is the same. Dynastic equivalence will be indicated by the equivalence relation $\sim$. Formally,

$$X_1 \sim X_2 \iff \forall L \subset \mathcal{S} : \Gamma_{X_1}^1(L) = \Gamma_{X_2}^1(L). \tag{91}$$

■

Example 39 (Uniform Crossover) Given a search space[4]

$$\mathcal{S} = \mathbb{Z}_k^n, \tag{92}$$

where $\mathbb{Z}_k$ is the set of integers (modulo k), the uniform crossover operator

$$\mathcal{U} : \mathbb{Z}_k^n \times \mathbb{Z}_k^n \times \mathbb{B}^n \longrightarrow \mathbb{Z}_k^n \tag{93}$$

is defined (cf. Syswerda, 1989) by

$$\mathcal{U}_i(x, y, m) \triangleq \begin{cases} x_i, & \text{if } m_i = 0, \\ y_i, & \text{otherwise.} \end{cases} \tag{94}$$

The control parameter m is a binary mask of length n, and each of the child's genes is taken from the first or second parent according to the corresponding bit in the mask.

■

Definition 36 clearly admits a very broad class of "recombination" operators. The aim of the present section is to impose conditions on recombination which might be thought to be helpful in ensuring effective genetic search. Perhaps the most obvious condition that one might wish to impose on a recombination operator is that when the two parents are the same, all offspring produced by recombination will be clones of the parents. Such a recombination operator will be said to be *pure*. More generally, if a set of formae has been defined, corresponding a set of to characteristics that are thought to be important in determining performance, one might require of recombination that the children it produces should share any characteristics that the parents share. This is the essence of the property of *respect*. The following definitions make these notions precise.

[4] In practice, it will more commonly be the representation space (the set of chromosomes or genotypes) that will be $\mathbb{Z}_n^k$, but the distinction is unimportant for the purposes of the present example.

Definition 40 (Purity) Let X be a recombination operator over a search space $\mathcal{S}$, having control set $\mathcal{K}_X$. Then X will be said to be *pure* if and only if all the offspring produced by X when the parents are identical are themselves identical to the parents:

$$\forall x \in \mathcal{S}\ \forall k \in \mathcal{K}_X :\ X(x, x, k) = x. \tag{95}$$

■

Definition 41 (Respect) Let Ξ be a set of formae defined over a search space $\mathcal{S}$ and let X be a recombination operator over $\mathcal{S}$ with control set $\mathcal{K}_X$. Then X will be said to *respect* the formae in Ξ if and only if all the offspring produced by X are members of each forma to which both parents belong:

$$\forall \xi \in \Xi\ \forall x \in \xi\ \forall y \in \xi\ \forall k \in \mathcal{K}_X :\ X(x, y, k) \in \xi. \tag{96}$$

■

Lemma 42 (Respect $\iff$ all children lie in their parents' similarity set) *A recombination operator X, with control set $\mathcal{K}_X$, defined over a search space $\mathcal{S}$, respects a set Ξ of formae if and only if all the solutions produced by recombination lie in the similarity set of their parents:*

$$\forall x \in \mathcal{S}\ \forall y \in \mathcal{S} :\ X(x, y, \mathcal{K}_X) \subset \Sigma(\{x, y\}). \tag{97}$$

Proof: If the two solutions x and y share membership of no forma then respect imposes no conditions, so only the case where they share membership of at least one forma need be considered. The proof is then direct:

$$\begin{aligned}
& \forall x \in \mathcal{S}\ \forall y \in \mathcal{S} :\ X(x, y, \mathcal{K}_X) \subset \Sigma(\{x, y\}) && (98)\\
\iff\ & \forall x \in \mathcal{S}\ \forall y \in \mathcal{S}\ \forall k \in \mathcal{K}_X :\ X(x, y, k) \in \Sigma(\{x, y\}) && (99)\\
\iff\ & \forall x \in \mathcal{S}\ \forall y \in \mathcal{S}\ \forall k \in \mathcal{K}_X :\ X(x, y, k) \in \bigcap \{\xi \in \Xi \mid x, y \in \xi\} && (100)\\
\iff\ & \forall \xi \in \Xi\ \forall x \in \xi\ \forall y \in \xi\ \forall k \in \mathcal{K}_X :\ X(x, y, k) \in \xi. && (96\text{ bis})
\end{aligned}$$

□

Corollary 43 (Respect of covering formae implies purity) *A recombination operator X, that respects a set $\Xi(\Psi)$ induced by a set Ψ of equivalence relations that covers a search space $\mathcal{S}$, is pure.*

Proof: If both parents are the same, then clearly they are in the same forma for each equivalence relation in Ψ. Respect therefore requires that all children lie in each of these formae. Since Ψ covers $\mathcal{S}$, this means that the child is identical to the parents.

□

Respect restricts the solutions that any pair of parents are allowed to produce under recombination, to ensure that common characteristics are preserved. It also seems important, however, that recombination be capable of *combining* characteristics of two parents, provided these characteristics are compatible; this, after all, is normally considered to be its *raison d'être*. The property of *assortment*, defined below, characterises recombination operators that are capable of generating children with arbitrary admixtures of their parents' genes. The remainder of the present section is based primarily on the twin notions of respect and assortment; the choice of the latter as a relevant criterion against which to measure recombination operators is discussed in section 7.

Definition 44 (Assortment) A recombination operator X, defined over a search space $\mathcal{S}$ and having control set $\mathcal{K}_X$, will be said to *assort* a set Ξ of formae, also defined over $\mathcal{S}$, if and only if

$$\forall \xi_1 \in \Xi \; \forall \xi_2 \in \Xi \; (\xi_1 \cap \xi_2 \neq \varnothing) \; \forall x_1 \in \xi_1 \; \forall x_2 \in \xi_2 : \; \Gamma_X(\{x_1, x_2\}) \cap \xi_1 \cap \xi_2 \neq \varnothing. \tag{101}$$

The assortment will be said to be *proper* if this property holds for $\Gamma^1_X(\{x_1, x_2\})$ as well as for $\Gamma_X(\{x_1, x_2\})$, i.e. if

$$\begin{aligned} & \forall \xi_1 \in \Xi \; \forall \xi_2 \in \Xi \; (\xi_1 \cap \xi_2 \neq \varnothing) \; \forall x_1 \in \xi_1 \; \forall x_2 \in \xi_2 : \\ & \qquad \Gamma^1_X(\{x_1, x_2\}) \cap \xi_1 \cap \xi_2 \neq \varnothing \qquad (102) \\ \iff \quad & \forall \xi_1 \in \Xi \; \forall \xi_2 \in \Xi \; (\xi_1 \cap \xi_2 \neq \varnothing) \; \forall x_1 \in \xi_1 \; \forall x_2 \in \xi_2 \; \exists \, k \in \mathcal{K}_X : \\ & \qquad (X(x_1, x_2, k) \in \xi_1 \cap \xi_2 \text{ or } X(x_2, x_1, k) \in \xi_1 \cap \xi_2) \, . \qquad (103) \end{aligned}$$

■

Definition 45 (Separability) A set Ξ of formae defined over a search space $\mathcal{S}$ will be said to be *separable* if and only if the conditions of respect and assortment of the formae in Ξ are compatible. Formally this can be expressed as follows:

$$\forall \xi_1 \in \Xi \; \forall \xi_2 \in \Xi \; (\xi_1 \cap \xi_2 \neq \varnothing) \; \forall x_1 \in \xi_1 \; \forall x_2 \in \xi_2 : \; \Sigma(\{x_1, x_2\}) \cap \xi_1 \cap \xi_2 \neq \varnothing. \tag{104}$$

An operator that simultaneously respects and assorts Ξ will be said to *separate* Ξ (and the formae in Ξ).

■

Observation 46 The definitions of respect, assortment and separability depend only upon the definition of formae, not equivalence relations or bases, and thus not on genes or alleles. If the term forma is relaxed to include *any* subset of the search space, without particular reference to any equivalence relation which might induce that subset as an equivalence class, this allows these notions to be applied even when genes have not been defined, provided that formae have.

■

Definition 47 (Gene Transmission) Let E be a basis for a set Ψ of equivalence relations over a search space $\mathcal{S}$. Then a recombination operator X over $\mathcal{S}$ will be said to be (strictly) transmitting if and only if each allele present in any child produced by X is present also in at least one of its parents. Formally, this is the requirement that

$$\begin{aligned} & \forall x, y \in \mathcal{S} \; \forall k \in \mathcal{K}_X \; \forall \varepsilon \in E : \; (\varepsilon(x, X(x, y, k)) = 1 \text{ or } \varepsilon(y, X(x, y, k)) = 1) \qquad (105) \\ \iff \quad & \forall x, y \in \mathcal{S} \; \forall k \in \mathcal{K}_X : \; X(x, y, k) \in \Gamma(\{x, y\}) \qquad (106) \end{aligned}$$

i.e. every child produced by X is equivalent to at least one of its parents under each basic equivalence relation, or equivalently, that each of the child's alleles is inherited from one or other parent.

■

Lemma 48 (Gene transmission implies respect) *Let E be the basis for a set Ψ of equivalence relations over a search space $\mathcal{S}$. Then if a recombination operator*

$$X : \mathcal{S} \times \mathcal{S} \times \mathcal{K}_X \longrightarrow \mathcal{S} \tag{107}$$

transmits the genes in E, it respects the formae in $\Xi(\Psi)$.

Proof: It has been shown in lemma 42 that respect amounts to the condition that all children lie in their parents' similarity set. Gene transmission is the requirement that all children lie in their parents' dynastic potential. The proof therefore follows immediately from lemma 35, which shows that similarity sets contain dynastic potentials.

□

Definition 49 (g-separability) A set $\Xi(\Psi)$ of formae induced by a set Ψ of equivalence relations defined over a search space $\mathcal{S}$ will be said to be *g-separable* if and only if the conditions of gene transmission and assortment with respect to Ψ are compatible. Formally,

$$\forall \xi_1 \in \Xi(\Psi)\ \forall \xi_2 \in \Xi(\Psi)\ (\xi_1 \cap \xi_2 \neq \varnothing)\ \forall x_1 \in \xi_1\ \forall x_2 \in \xi_2 : \Gamma(\{x_1, x_2\}) \cap \xi_1 \cap \xi_2 \neq \varnothing. \tag{108}$$

■

Lemma 50 (g-separability implies separability) *Let Ψ be a set of equivalence relations over a search space $\mathcal{S}$. Then if $\Xi(\Psi)$ is g-separable, $\Xi(\Psi)$ is separable.*

Proof: This follows immediately from lemma 35, which shows that similarity sets contain dynastic potentials.

□

Definition 51 ($\Xi^\star$) Following from the definitions of Ξ_ψ and Ξ_Ψ given in definition 5, this notation is now extended to define $\Xi^\star_\psi$ and $\Xi^\star_\Psi$ as follows. Given $\psi \in \Psi \subset \mathbb{E}(\mathcal{S})$, let

$$\Xi^\star_\psi \triangleq \Xi_\psi \cup \{\mathcal{S}\} \tag{109}$$

and

$$\Xi^\star_\Psi \triangleq \prod_{\psi \in \Psi} \Xi^\star_\psi. \tag{110}$$

■

Lemma 52 (Representations of Formae) *Let E be an n-dimensional orthogonal basis for a set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$. Then every forma ξ induced by a relation $\psi \in \Psi$ can be expressed uniquely as the product of the components of some member $\boldsymbol{\xi} \in \Xi^\star_E$. Formally,*

$$\forall \xi \in \Xi(\Psi)\ \exists ! \boldsymbol{\xi} \in \Xi^\star_E : \bigcap_{i=1}^{n} \xi_i = \xi, \tag{111}$$

where $\exists !$ is read "there exists a unique", and $\boldsymbol{\xi} = (\xi_1, \xi_2, \ldots, \xi_n)$.

Proof: Let ξ be induced by the equivalence relation $\psi \in \Psi$, i.e. $\xi \in \Xi_\psi$. Then since E is a basis for Ψ,

$$\exists\, A_\psi \subset E : \bigcap A_\psi = \psi. \tag{112}$$

The existence of a $\boldsymbol{\xi}$ satisfying equation 111 follows fairly directly from lemma 8, which showed that the formae induced by intersections of equivalence relations are intersections of the formae induced by the "parent" relations. Making appropriate substitutions, equation 23 becomes

$$\forall \xi \in \Xi_\psi\ \exists\, \boldsymbol{\xi}' \in \Xi_{A_\psi} : \bigcap_{i=1}^{|A_\psi|} \xi'_i = \xi, \tag{113}$$

where $\boldsymbol{\xi} = (\xi_1, \xi_2, \ldots, \xi_{|A_\psi|})$. The vector $\boldsymbol{\xi}' \in \Xi_{A_\psi}$ can be extended to a $\boldsymbol{\xi} \in \Xi^\star_E$ simply by setting the "extra" components of $\boldsymbol{\xi}$ (those corresponding to those relations $\varepsilon \in E \setminus A_\psi$) to $\mathcal{S}$. Clearly then

$$\bigcap_{i=1}^{n} \xi_i = \xi \tag{114}$$

also, since the only "extra" intersections compared with $\boldsymbol{\xi}'$ are those with $\mathcal{S}$.

Uniqueness for the components of ξ corresponding to relations in A_ψ follows from the fact that the equivalence classes induced by any equivalence relation are disjoint. That the remaining components of $\boldsymbol{\xi}$ can only be $\mathcal{S}$ follows from the orthogonality of E.

□

Lemma 53 (Respect $\Longleftrightarrow$ Children include all alleles common to their parents) *Let $\Xi(\Psi)$ be a set of formae induced by a set Ψ of equivalence relations over a search space $\mathcal{S}$. Then a recombination operator*

$$X : \mathcal{S} \times \mathcal{S} \times \mathcal{K}_X \longrightarrow \mathcal{S} \tag{115}$$

respects $\Xi(\Psi)$ if and only if the alleles common to the parents are present in every child produced by X.

Proof: This is immediately clear because every equivalence relation $\psi \in \Psi$ can be expressed as an intersection of basic equivalence relations in E, and thus every equivalence class (forma) $\xi \in \Xi(\Psi)$ can be expressed as an intersection of basic formae in $\Xi(E)$, by lemma 52. Clearly, therefore, if $\Xi(E)$ is respected, (i.e. every allele common to the parents is included in all children produced by X) then all their intersections must be respected also. □

Example 54 (Schemata are g-separable) Let

$$\mathcal{S} = \mathbb{Z}_k^n, \tag{116}$$

the set of k-ary strings of length n, and let Ξ be the corresponding set of schemata:

$$\Xi = (\mathbb{Z}_k \cup \{\square\})^n \tag{117}$$

where $\square$ is the "don't care" character. Then Ξ is g-separable, and uniform crossover (see definition 39) both transmits genes and assorts schemata. To see this, observe first, from lemma 53, that in this case respect amounts to the requirement that all alleles present in the child come from one or other parent, and that uniform crossover plainly ensures this. Moreover, assortment now amounts to the requirement that any combination of the parents alleles be capable of being produced, and uniform crossover also ensures this. Thus uniform crossover transmits and assorts schemata, so schemata are g-separable.

■

Example 55 (Non-separable formae) Let $\mathcal{P}_n$ be the set of permutations of the elements of $\mathbb{Z}_n$. Then given a set $\mathcal{E}$ of undirected edges that it is possible for a permutation to include, (an edge specifying the adjacency of two elements in the permutation) let the forma $\xi_{\mathcal{E}}$ be the set of all permutations that include the edges in $\mathcal{E}$. The set Ξ of all such formae is non-separable. To see this, observe that if a permutation x contains the sub-permutation 1–2–3 and another permutation y contains the sub-permutation 1–2–4, respect requires that the 1–2 edge be contained in all the offspring produced by recombination of x and y, while assortment requires that recombining them allows the generation of a permutation containing both the 2–3 and the 2–4 edges. Clearly these requirements are incompatible.

■

Corollary 56 (Orthogonal formae are isomorphic to schemata) *Let E be an n-dimensional orthogonal basis for a set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$ that covers $\mathcal{S}$, and assume that Ψ is closed under intersection. Then the formae in $\Xi(\Psi)$ are isomorphic to schemata with genes E and alleles $\Xi(E)$.*

Proof: Lemma 52 has already shown that any forma in $\Xi(\Psi)$ can be expressed as an intersection of the components of a vector $\boldsymbol{\xi} \in \Xi_E^\star$. It has previously been argued that basic formae are the natural generalisation of alleles, and this only leaves the identification of "intersecting with $\mathcal{S}$" with the "place-holder" wildcard $\square$. This is clearly also very natural: intersecting with $\mathcal{S}$ does not narrow the membership of a forma at all, and similarly including a "don't care" character allows any allele to occupy that position, thus not narrowing the solutions contained within a schema.

□

Theorem 57 (Orthogonality implies g-separability) *Let E be an orthogonal basis for a set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$. Then $\Xi(\Psi)$ is g-separable.*

Proof: This follows immediately from corollary 56 since schemata have already been shown to be g-separable (example 54).

□

Observation 58 (Non-orthogonality does not imply non-separability) The fact that a set of formae is non-orthogonal does not mean that it is necessarily non-separable. An example of a set of separable formae induced by non-orthogonal genes can be found in Radcliffe (1991a, 1992a).

■

Having now defined a number of properties—purity, respect, gene transmission and assortment—that appear to be relevant to genetic search, it is natural to try to identify generic operators that satisfy these properties. The following definitions introduce a family of three related operators, known as *random respectful recombination*, (R^3), *random transmitting recombination* (RTR) and *random assorting recombination* (RAR). These three operators are related, and all reduce to uniform crossover in the case of binary schemata. They are subtly different in cases of non-separable formae, and in cases where genes are non-orthogonal. Each has proved useful in some practical applications (Good, 1993; Jones, 1992; Shapcott, 1992). The simplest of the operators is R^3, which, as the following definition shows, delivers a child that is randomly selected from the parents' similarity set.

Definition 59 (Random Respectful Recombination (R^3)) Given a set Ξ of formae over a search space $\mathcal{S}$, the *random respectful recombination operator*

$$R^3 : \mathcal{S} \times \mathcal{S} \times \mathbb{Z} \longrightarrow \mathcal{S} \tag{118}$$

is defined by

$$R^3(x, y, k) = \sigma_{k'}(x, y) \tag{119}$$

where $\sigma_i(x, y)$ is the ith element of the similarity set of x and y under some arbitrary enumeration and $k' \triangleq k \pmod{|\Sigma(\{x, y\})|}$. Thus if R^3 is given a random control parameter, it returns a randomly-selected member of the parents' similarity set.

■

Corollary 60 (R^3 respects) *Random respectful recombination respects the formae with respect to which it is defined.*

Proof: This follows immediately from lemma 42, (which shows that respect amounts to requirement that children lie in their parents' similarity set) since R^3 selects children only from the similarity set of the parents.

□

Theorem 61 (R^3 separates separable formae) *Let Ξ be a separable set of formae over a search space $\mathcal{S}$. Then R^3 (defined with respect to Ξ) separates Ξ.*

Proof: First notice that R^3 generates every solution in the similarity set of the parents given suitable control parameters. This is, from lemma 42, the maximal set of offspring compatible with respect. Thus if R^3 cannot assort the formae in Ξ, nor can any other respectful recombination operator. Thus R^3 respects and assorts any separable set of formae.

□

R^3 is unusual in that it does not, in general, restrict children's alleles to be inherited from their parents. The RTR operator, defined next, adds this restriction.

Definition 62 (Random Transmitting Recombination (RTR)) Given a basis E for a set Ψ of equivalence relations over a search space $\mathcal{S}$, the *random transmitting recombination* operator

$$\text{RTR} : \mathcal{S} \times \mathcal{S} \times \mathbb{Z} \longrightarrow \mathcal{S} \tag{120}$$

is defined by

$$\text{RTR}(x, y, k) \triangleq \gamma_{k'}(x, y) \tag{121}$$

where $\gamma_i(x, y)$ is the ith member of the dynastic potential $\Gamma(\{x, y\})$ of the parents x and y under some arbitrary enumeration of $\Gamma(\{x, y\})$, and $k' \triangleq k \pmod{|\Gamma(\{x, y\})|}$. Thus if RTR is given a randomly selected control parameter, it returns a random member of the parents' dynastic potential.

■

Theorem 63 (RTR transmits and assorts g-separable genes) *Let E be the basis for a set $\Psi \subset \mathbb{E}(\mathcal{S})$ of equivalence relations over a search space $\mathcal{S}$. Then RTR transmits the genes in E and assorts them if they are g-separable.*

Proof: That RTR transmits genes follows immediately from the definition, since the dynastic potential of a pair of parents is precisely those children that can be constructed only from their genes. It therefore remains only to show that RTR assorts the genes in E. This is also obvious, because the span of RTR is the whole dynastic potential of the parents, and thus it generates every solution that is compatible with gene transmission. Thus if RTR fails to assort the formae in $\Xi(\Psi)$, it is clear that no transmitting recombination operator can do so, and thus they are not g-separable.

□

Theorem 64 (RTR $\sim$ uniform crossover given orthogonal genes) *Let E be an orthogonal basis for a set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$. Then RTR is dynastically equivalent to uniform crossover.*

Proof: The dynastic span of RTR is, by definition, the dynastic potential of the parents, and orthogonality ensures that all combinations of the parents genes represent legal solutions. It therefore suffices to show that

$$\forall x, y \in \mathcal{S} : \ \Gamma_{\mathcal{U}}(\{x, y\}) \equiv \Gamma(\{x, y\}). \tag{122}$$

Since uniform crossover is defined precisely to produce a child by selecting the value for each gene at random from the values of the parents, this is clearly the case.

□

Theorem 65 (For orthogonal binary genes, $\mathbf{R}^3 \sim$ RTR) *Let E be an orthogonal basis for a set of equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$. Then if each gene in E is binary (has precision 2), R^3 is dynastically equivalent to RTR.*

Proof: This follows as an immediate consequence of the fact that if the parents have different alleles (i.e. are in different basic formae) for some gene, the range of values RTR allows is still the entire allele set since there are only two alleles.

□

Having introduced R^3 and RTR, recombination operators that give primacy to the related characteristics of respect and gene transmission respectively, the final operator that will be introduced, random *assorting* recombination (RAR_w), sacrifices these in favour of assortment when the principles are in conflict. It does so, however, in a parameterised way, so that the trade-off between respect and assortment can be controlled. The essential idea behind the operator is to collect together all the alleles present in the parents in a bag. The number of copies of an allele placed in the bag depends on whether or not it is common to the two parents. (There are w

times as many copies of common alleles as of those present only in one parent.) Alleles are then randomly drawn from the bag, without replacement, and placed in the forming child, provided that they are not incompatible with alleles already chosen for it. Such an incompatibility will obviously arise if a different allele has already been selected for the child's corresponding gene. If the basis is non-orthogonal, however, it may also arise simply because of an incompatibility between alleles at different loci. This initial phase of the operator completes either when the child is fully specified, or when the bag is empty. In the latter case, the operator completes the child by making random (legal) assignments to the unspecified genes in the child, taking appropriate account of any incompatibilities that may arise from non-orthogonal genes.

The following definitions give a more precise formulation of the operator.

Definition 66 (Multiplicity m) Let $\mathcal{M}$ be a multiset (bag), i.e. a collection of elements in which repetition of members is significant. Then define the multiplicity $m(x, \mathcal{M})$ of a member x in $\mathcal{M}$ to be the number of copies x in $\mathcal{M}$.

■

Definition 67 (Random Assorting Recombination (RAR$_w$)) Let E be a basis for a set Ψ of equivalence relations that cover a search space $\mathcal{S}$. Then

$$\mathrm{RAR}_w : \mathcal{S} \times \mathcal{S} \longrightarrow \mathcal{S} \tag{123}$$

is a recombination operator that constructs a child $\mathrm{RAR}_w(x, y)$, (w integral), from parents x and y as follows. Construct a multiset $\mathcal{B}_0$ of alleles by

$$\forall \xi \in \Xi(E) : m(\xi, \mathcal{B}_0) \triangleq \begin{cases} w, & \text{if } x, y \in \xi, \\ 1, & \text{if } x \in \xi \text{ xor } y \in \xi, \\ 0, & \text{otherwise.} \end{cases} \tag{124}$$

Further, define a set $\mathcal{R}_0 \triangleq \mathcal{S}$. Now recursively define the multisets $\mathcal{B}_i$ by picking a random member ξ_i from $\mathcal{B}_{i-1}$ and setting

$$\mathcal{B}_i \triangleq \mathcal{B}_{i-1} \setminus [\![\xi_i]\!], \tag{125}$$

(where $[\![\cdots]\!]$ denotes a multiset) and then recursively define the sets $\mathcal{R}_i$ by

$$\mathcal{R}_i \triangleq \begin{cases} \mathcal{R}_{i-1} \cap \xi_i, & \text{if } \mathcal{R}_{i-1} \cap \xi_i \neq \varnothing, \\ \mathcal{R}_{i-1}, & \text{otherwise.} \end{cases} \tag{126}$$

Continue these recursive definitions until step n, at which $\mathcal{B}_n = \varnothing$. Then let $\mathrm{RAR}(x, y)$ be a randomly chosen member of $\mathcal{R}_n$.

Notice that this definition, as presented, does not have an explicit control set, and thus does not conform to the standard form of recombination operator suggested in definition 36. This is easily effected, however, by introducing an (arbitrary) enumeration over $\mathcal{R}_n$ and using $\mathbb{Z}$ as a control set, with the integer control parameter (mod $|\mathcal{R}_n|$) being used to select the member of $\mathcal{R}_n$ chosen.

■

Note that the above definition is intended as a formal construction of RAR only, and is unlikely ever to be an efficient method for its implementation. Notice further, that the higher the value of w, the higher is the probability that RAR$_w$ will respect, because the more copies of the common alleles will be present in the bag.

The weight parameter, w, determines the relative probability, during the first phase of RAR$_w$'s operation, of picking alleles that are common to the two parents rather than those that are present only in one. Higher values of w bias the operator more strongly towards choosing common alleles, encouraging respect. Indeed as w is increased, the distribution of solutions produced by RAR$_w$ clearly approaches that of R^3. Conversely, lower values lead to less emphasis on common alleles and respect, but encourage more assortment.

It is a simple matter to generalise the operator to accept any non-negative weight w, rather than integral values only. In this case, values of w less than one actively bias the operator *against* common alleles, encouraging very strong mixing of the alleles that differ between the parents. Experiments with a range of values for w above and below one are described in Radcliffe & George (1993).

The following theorem confirms, as expected, that for any finite value of w, RAR$_w$ assorts.

Theorem 68 (RAR assorts) *Let E be a basis for a set of equivalence relations $\Psi \subset \mathbb{E}(\Psi)$. Then for all values of $w \in \mathbb{Z}^+$, RAR$_w$ properly assorts the formae in $\Xi(\Psi)$.*

Proof: Recall the definition of proper assortment (equation 102), applied to this case is as follows:

$$\forall \xi_1 \in \Xi \; \forall \xi_2 \in \Xi \; (\xi_1 \cap \xi_2 \neq \varnothing) \; \forall x_1 \in \xi_1 \; \forall x_2 \in \xi_2 : \; \Gamma^1_{\mathrm{RAR}_w}(\{x_1, x_2\}) \cap \xi_1 \cap \xi_2 \neq \varnothing. \tag{127}$$

Lemma 8 shows that ξ_1 and ξ_2 can be represented as intersections of basic equivalence relations in $\Xi(E)$ since E is a basis for Ψ. Thus

$$\exists A_1 \subset \Xi(E) : \bigcap A_1 = \xi_1 \tag{128}$$

and

$$\exists A_2 \subset \Xi(E) : \bigcap A_2 = \xi_2. \tag{129}$$

Clearly

$$(\cap A_1) \cap (\cap A_2) \equiv \bigcap (A_1 \cup A_2) = \xi_1 \cap \xi_2. \tag{130}$$

Each member of A_1 is an allele that the parent x_1 contains, and similarly each member of A_2 is an allele that the parent x_2 contains. Moreover, since $\xi_1 \cap \xi_2$ is by assumption non-empty, all the alleles in $A_1 \cup A_2$ are compatible. Examining definition 67 (the definition of RAR$_w$), it is clear that each allele in $A_1 \cup A_2$ will be in the bag $\mathcal{B}_0$ of available alleles with multiplicity strictly greater than zero. It is therefore possible that each of these alleles will be selected before any others, and that if this happens, they will all be found to be compatible (because they are!). This suffices to show that RAR$_w$ can generate a solution in the intersection as required.

□

Theorem 69 (RAR transmits and assorts g-separable genes) *Let E be a basis for a covering set of g-separable equivalence relations $\Psi \subset \mathbb{E}(\mathcal{S})$. Let Ψ be closed under intersection, i.e.*

$$\forall \psi, \phi \in \Psi : \; \psi \cap \phi \in \Psi. \tag{131}$$

Then for all values of $w \in \mathbb{Z}^+$, RAR$_w$ assorts and transmits the genes in E.

Proof: Theorem 68 has already shown that RAR$_w$ assorts the genes in E, so it remains only to show that it transmits them also when these two conditions are compatible. Continuing from the proof of theorem 68, observe first that if by the time the bag of alleles is empty the child has been fully specified, then RAR$_w$ would indeed have transmitted, because all the child's alleles would then have come from one or other parent. Since E covers Ψ, the child could only fail to be fully specified after the bag has been emptied if for some gene neither of the parents' corresponding alleles were found to be compatible with the other alleles already selected. To complete the proof, therefore, it suffices to show that this would contradict g-separability.

Suppose, then, that after partially constructing the child using RAR$_w$, it became impossible to include the allele from either parent for some gene ε. Let the forma ξ denote the intersection of all those alleles that the (partial) child possesses at this stage. Then clearly no recombination operator which could construct a child in ξ could strictly transmit genes. The forma ξ, however, is non-empty by construction (see definition 67). Let the parent solutions be x_1 and x_2. Since ξ is an intersection of alleles from these parents, it is clear that there must be formae ξ_1 and ξ_2, with $x_1 \in \xi_1$ and $x_2 \in \xi_2$, such that $\xi_1 \cap \xi_2 = \xi$. Since ξ is non-empty, assortment requires

that a recombination operator be capable of generating a solution in ξ. Thus if membership of ξ is incompatible with gene transmission, the genes cannot be g-separable, contradicting the assumption and completing the proof.

□

Definition 70 (Hill-climber) Given a search space $\mathcal{S}$, for the purposes of the current paper, a hill-climber will be defined as any function

$$h : \mathbb{P}(\mathcal{S}) \longrightarrow \mathcal{S}. \tag{132}$$

Thus given a set of solutions, a hill-climber picks one of them.

■

It will normally be helpful, and accord better with common usage of the term hill-climber, if h returns at least a local maximum (with respect to some move operator or metric) from the set that forms its argument.

Example 71 (Enumeration) Simple deterministic hill-climbing is an example of a hill-climber in the sense of definition 70. Enumeration evaluates every solution in the given subset of $\mathcal{S}$ and returns the one with the highest fitness. In the case where there is more than one such point, an arbitrary choice is made.

■

Definition 72 (Random Assorting Recombination with Hill-climbing (RAR$_{wh}$)) The *random assorting recombination operator with hill-climber h* (RAR$_{wh}$) is an extension of RAR$_w$ that depends on the existence of a hill-climber h. The definition of RAR$_{wh}$ is identical to that of RAR$_w$ until $\mathcal{R}_n$ has been constructed (i.e. the bag of alleles is empty). Instead of making a random selection from the children in $\mathcal{R}_n$, RAR$_{wh}$ applies the hill-climber h to $\mathcal{R}_n$ and returns its result this as the child produced.

■

Theorem 73 (Orthogonality implies RAR$_w$ is dynastically equivalent to RTR) *Let E be an orthogonal basis for a set Ψ of equivalence relations that covers a search space $\mathcal{S}$. Then RAR$_w$ and RTR (defined with respect to E and $\Xi(\Psi)$) are dynastically equivalent:*

$$\forall w \in \mathbb{Z}^+ : \mathit{RAR}_w \sim \mathit{RTR}. \tag{133}$$

Proof: Recall that orthogonality amounts precisely to the requirement that any combination of alleles from different genes should be present in some solution in $\mathcal{S}$. It is clear that the only circumstances in which it will be impossible to place an allele in a child will be those in which a different allele has already been chosen for that gene. It is also clear that by the time the sequence of bags $\mathcal{B}_i$ is empty the child will have been fully specified because one allele will have been assigned for each gene. Thus all combinations of the parents' genes will be capable of being produced by RAR, and all children will consist solely of alleles selected from the parents. This shows that given orthogonal genes, the dynastic span of RAR$_w$ is equal to the dynastic potential of any set of parents. Since this is also the case for RTR, the two must be dynastically equivalent.

□

Corollary 74 (RAR$_w$ transmits and assorts orthogonal formae) *Let E be an orthogonal basis for a set $\Psi \subset \mathbb{E}(\mathcal{S})$ of equivalence relations over a search space $\mathcal{S}$. Then for all values of w, RAR transmits and assorts the genes in E.*

Proof: Since orthogonal genes are g-separable by theorem 57 and RTR transmits and assorts them by theorem 63, the result follows immediately from the previous theorem, which shows that RAR$_w$ is dynastically equivalent to RTR for orthogonal formae.

□

7 Discussion

The preceding sections have formalised many of the earlier results of forma analysis and proved for the first time a number of relationships between the structure of patterns of correlations in a search space and the manipulations that it is possible to perform on the members of the search space. The purpose of the present section is to set these in context, and to discuss the relationship between the approach of forma analysis, in which operators are designed to achieve specific effects, and the more common approach suggested by schema analysis, whereby a representation is constructed to allow "standard" operators to manipulate solutions.

Forma analysis provides a method for constructing operators and representations using the mechanism of codifying such knowledge as the worker has through equivalence relations or through the explicit construction of alleles. Each member of the suggested family of operators manipulates solutions so as to achieve purity, respect, gene transmission and assortment in various measures. These notions have been arrived at by studying the way conventional crossover operators manipulate schemata. In the context of schemata, the principles of gene transmission and proper assortment restrict the set of available operators to those that are dynastically equivalent to uniform crossover. Because it chooses each of the children within the dynastic potential of the parents with equal probability, uniform crossover may be regarded as a "neutral" operator that may be refined by biasing it in various ways. For example, Eshelman *et al.* (1989) have helpfully characterised recombination operators in terms of *positional* and *distributional* bias. Positional bias refers to the tendency of operators to distinguish between alleles chosen for propagation from one parent to the child on the basis of their positions on the chromosome. Thus, one-point crossover is highly positionally biased, because adjacent alleles are very much more likely to be transmitted together than distant alleles. Uniform crossover, on the other hand, exhibits no positional bias because any pair of alleles is equally likely to be transmitted whole. The characteristics of R^3, RTR and RAR_w are the same as those of uniform crossover in this regard. Positional bias as demonstrated by one-point crossover is helpful in many problems because representations are often chosen which link strongly interacting genes by placing them in close proximity on the chromosome; this is particularly helpful when the genes exhibit epistasis.

It should be recalled, however, that Holland (1975) originally proposed that one-point crossover be used in conjunction with a re-linking operator (inversion) which would move genes around the chromosome to allow the search to discover strong linkages adaptively. If the linkage of a chromosome is regarded as a random variable, this restores n-point crossover to the status of properly assorting; moreover, insofar as the linkage is actually non-random, it would be presumed that adaptation would concentrate assortment on fruitful areas of the genome. Despite some effort, however, studies including those by Cavicchio (1970), Franz (1972) and Radcliffe (1990) have failed to observe significant improvements in performance using inversion. Bethke (1970) has attributed the failure of the early studies to demonstrate a significant effect to the simplicity of problems studied. It is possible, however, that the selective pressure exerted by superior linkage may be too weak to be usefully exploited in most applications. (This suspicion motivated the formulation of the PMX operator by Goldberg & Lingle (1985) as a sexual re-linking operator, though the author is unaware of any experiments with this idea to date.) It is also possible that the perceived superiority of n-point crossover on many problems discussed in the literature may stem in part from the concentration on tackling real parameter optimisation problems using a binary coding in which there is clearly strong linkage between the many adjacent bits that code a single parameter. It is therefore rather unclear whether the positionally unbiased nature of R^3, RTR and RAR_w should in general be regarded as a benefit or a weakness.

Distributional bias refers to the tendency of an operator to choose the amount of genetic material to be drawn from one parent other than uniformly. One-point crossover thus exhibits no distributional bias (assuming the cross point is itself picked uniformly) while uniform crossover (with parameter half) exhibits a strong bias towards taking half the material from each

parent. It is easy, however, to control the distributional bias for most operators by changing the distributions from which their control parameters are drawn. Spears & DeJong (1991) have used this freedom to manipulate the distributional characteristics of recombination operators and show that if a parameter other than half is picked for uniform crossover (so that there is a bias towards taking material from a preferred parent) then its much-criticised disruptive effect on schema membership can be controlled. This important point has rather wide applicability. For example, RAR_w can trivially be biased towards one parent simply by placing k additional copies of all alleles from that parent in the bag at the outset.

Taken together, these points suggest that R^3, RTR and RAR_w should not be viewed as "ideal" operators, but merely as neutral operators akin to uniform crossover. They may be further refined, for example by manipulating the distribution from which control parameters are selected, by biasing the content of the bag (in the case of RAR_w) and possibly even by adding an explicit notion of linkage which could then be used to construct "n-point crossover-like" variations of, for example, RAR_w.

Having placed the discussions in the paper in a clearer context, it is perhaps worth discussing in a little more detail why, as well as all the above considerations, assortment may be a property of some significance for a recombination operator. It has already been shown that situations can arise in which respect (or strict gene transmission) is not compatible with assortment, and that most of the standard operators respect schemata (and strictly transmit genes). Practical examples in which the principles are incompatible using natural formae include the travelling sales-rep problem (Radcliffe, 1991b, where the formae are based on directed or undirected edges), neural network topology optimisation (Radcliffe, 1993, where they are based on nodes) and fixed-size set and multiset problems (Radcliffe, 1992a, where they are based on set membership). Thus if a respectful operator is used, the non-separability immediately means that assortment must fail to be achieved. The significance of this is that even when parents are chosen that contain all the genetic material (apparently) necessary to build some given child, it may be impossible for a respectful recombination operator to construct that child. As well as being in conflict with reason, this would seem to make navigation around the search space unnecessarily difficult.

It is hoped that these discussions suffice to show that the principles discussed, (purity, respect, assortment and transmission) far from being arbitrary, precisely capture the behaviour of standard crossover operators on separable problems. The virtue of formulating the principles explicitly is that this permits them to be applied and analysed in domains in which solutions are not naturally expressed as linear strings of genes that may be independently assigned.

Among the more important results that have been shown in this paper, the existence of a unique genetic representation given a set of equivalence relations (theorem 29) stands out. This requires careful interpretation. The mathematical content of the theorem is simply that given any set of equivalence relations over a search space, it is possible to construct a unique basis (a minimal subset out of which the remainder may be constructed) for those relations. If, however, the identification of basic equivalence relations with genes and of basic formae with alleles is accepted, this means that given a set of relations that covers a search space $\mathcal{S}$, there is exactly one (abstract) genetic representation consistent with the characterisation expressed by those equivalence relations. If it is further accepted that respect, assortment and so forth are the relevant characteristics of effective genetic recombination operators, then R^3, RTR and RAR suggest themselves at least as natural starting points for recombination operators.

The relationships between general formae and schemata have also been clarified in this paper, as have the relationships between R^3, RTR and RAR. The formae induced by a set of equivalence relations with a covering orthogonal basis are isomorphic to schemata: thus orthogonal genes are the standard case that workers in the field have become accustomed to thinking about. Moreover, given orthogonal formae, both RTR and RAR reduce to uniform crossover. (If the genes are binary, R^3 so-reduces also.) One of the important uses of forma analysis, therefore, is to allow analysis of cases in which non-orthogonal (but possibly separable) and non-separable

formae are involved.

The approach taken in forma analysis is to make explicit those characteristics of solutions that are considered to be important in determining performance, to encapsulate these through equivalence relations (or at least through formae) and then to construct operators that manipulate these characteristics (formae, genes) in line with the notions of purity, respect, gene transmission and assortment, as appropriate and feasible. An alternative, and more conventional approach, is to seek to construct a linear string representation in which schemata are meaningful and then to use "standard" operators (typically n-point or uniform crossover). It has, of course, already been demonstrated that uniform crossover transmits and properly assorts the genes associated with schemata; n-point crossover, for fixed n, transmits and weakly assorts genes.

At first sight it may seem that these two approaches are equivalent. It is easy to imagine that there might be a *duality* between operators and representations, in the sense that any desired manipulations could be achieved either by fixing the operator (say uniform or 1-point crossover) and manipulating the representation, or by fixing the representation and varying the operator. A more careful examination shows that this is not so.

The first clarification concerns "representations". Under the conventional approach, recombination operators are defined explicitly with respect to the genetic encoding. Thus a recombination operator is viewed as taking two *genotypes* (chromosomes), together with a control parameter, and producing another genotype. Throughout this paper, and the more recent of the previous papers on forma analysis, this has been avoided: instead recombination operators have been defined directly in the *phenotype* space—the given search space $\mathcal{S}$. Thus with forma analysis the *phenotypic* effect of operators is specified and the encoding used is left as a matter for the implementor. (This is similar to the way in which a mathematician will specify the meaning of multiplication, and leave as an implementation decision the choice of floating point representation: multiplication is unchanged provided that the effect of multiplying two numbers is independent of the encoding chosen.)

In this sense, the choice of representation (i.e. encoding) of phenotypes in $\mathcal{S}$ does not alter the (phenotypic) effect of an operator specified in phenotypic terms. This encoding independence should not distract, however, from the way in which the imposition of a set of equivalence relations that covers a search space, and the subsequent extraction of the basis for those relations, corresponds at a more fundamental level to the definition of genes and alleles, and thus specifies an "abstract representation".

In considering the set of all possible recombination operators over a search space $\mathcal{S}$, it is not useful for present purposes, to distinguish between operators that are dynastically equivalent. It therefore suffices to consider all the different sets of children that may be produced by each pair of parents. The set R_0 of dynastically non-equivalent operators is

$$R_0 \triangleq \mathbb{P}(\mathcal{S})^{\mathcal{S}_2}, \tag{134}$$

where $\mathcal{S}_2$ is the set of unordered pairs of (parent) solutions in $\mathcal{S}$,

$$\mathcal{S}_2 \triangleq \left\{ \{x, y\} \;\middle|\; x, y \in \mathcal{S} \right\} \tag{135}$$

and $\mathbb{P}(\mathcal{S})^{\mathcal{S}_2}$ is the set of all mappings from pairs of solutions in $\mathcal{S}$ to subsets of $\mathcal{S}$:

$$\mathbb{P}(\mathcal{S})^{\mathcal{S}_2} \triangleq \left\{ f \;\middle|\; f : \mathcal{S}_2 \longrightarrow \mathbb{P}(\mathcal{S}) \right\}. \tag{136}$$

Similarly, In considering the set of all encodings of a search space $\mathcal{S}$, assuming that only faithful representations are considered (i.e. those for which each solution has exactly one chromosomal representative, and that representatives are distinct) the set of representations is

$$R_1 \triangleq \left\{ r : \mathcal{S} \longrightarrow \mathcal{C} \;\middle|\; r \text{ is bijective} \right\}, \tag{137}$$

where $\mathcal{C}$ is an arbitrary set of the same size as $\mathcal{S}$. If $|\mathcal{S}| = N$, then the size of R_0 is given by

$$|R_0| = |\mathbb{P}(\mathcal{S})|^{|\mathcal{S}_2|} \quad (138)$$

$$= (2^N)^{N(N-1)/2}. \quad (139)$$

The size of R_1, the number of different invertible encodings of $\mathcal{S}$, is only

$$|R_1| = N! < N^N < (2^N)^N < (2^N)^{N(N-1)/2} = |R_0|. \quad (140)$$

It should therefore be clear that there is no duality between representations and operators (because $|R_1| \ll |R_0|$). It is, moreover, obvious that any manipulations that can be achieved with a "standard" operator on a linear string representation can be produced by an abstract operator that has the same phenotypic effects given an arbitrary representation. Thus the approach of fixing the operator is more restrictive than that pursued here. (It is of course possible to establish a duality between representations and a suitable subset of operators, and this is often useful, but it is not the aim of the present paper.)

The fact that more operators may be considered is not, of course, an intrinsic virtue, and is useful only if some of the operators not usually available to schema analysis are useful. Some cases in which there is reason to believe this might be so have been discussed previously in Radcliffe (1992b). In summary these are problems for which

- the genes are non-orthogonal, but are separable, in which case R^3 or RTR may be of use;
- the formae are non-separable, in which case it may be desirable to use an operator such as RAR_w or RAR_{wh};
- the size of the search space $\mathcal{S}$ is not a power of a convenient small integer (particularly 2), so that no simple string representation is available.

It is also often easier to manipulate entities whose natural computer representation is redundant in a more satisfactory manner using this approach. Notice also that since RAR_w has been shown to be equivalent to uniform crossover when the basis for the chosen set of equivalence relations is orthogonal, there is a sense in which RAR_w is a completely general operator that behaves appropriately both in the "standard" case (orthogonal genes) and in the context of more exotic problems.

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References

Antonisse, 1989. Jim Antonisse. A new interpretation of schema notation that overturns the binary coding constraint. In *Proceedings of the Third International Conference on Genetic Algorithms*. Morgan Kaufmann (San Mateo), 1989.

Bethke, 1970. A. D. Bethke. *Genetic Algorithms and Function Optimizers*. PhD thesis, Univerity of Michigan, 1970.

Bridges and E., 1987. C. Bridges and Goldberg D. E. An analysis of reproduction and crossover in a binary-coded genetic algorithm. In *Proceedings of the Second International Conference on Genetic Algorithms*. Lawrence Erlbaum Associates (Hillsdale, New Jersey), 1987.

Cavicchio, 1970. D. J. Cavicchio. *Adaptive Search Using Simulated Evolution*. PhD thesis, Univerity of Michigan, 1970.

Eshelman *et al.*, 1989. Larry J. Eshelman, Richard A. Caruana, and J. David Schaffer. Biases in the crossover landscape. In *Proceedings of the Third International Conference on Genetic Algorithms*. Morgan Kaufmann (San Mateo), 1989.

Franz, 1972. D. R. Franz. *Non-linearities on Genetic Adaptive Search*. PhD thesis, Univerity of Michigan, 1972.

Goldberg and Lingle Jr, 1985. David E. Goldberg and Robert Lingle Jr. Alleles, loci and the traveling salesman problem. In *Proceedings of an International Conference on Genetic Algorithms*. Lawrence Erlbaum Associates (Hillsdale), 1985.

Good, 1993. Steven Good. Applying a genetic algorithm to a high frequency detector location problem. Technical Report (final year), Department of Computer Science, University of Edinburgh, 1993.

Holland, 1975. John H. Holland. *Adaptation in Natural and Artificial Systems*. University of Michigan Press (Ann Arbor), 1975.

Jones, 1992. Graham P. Jones. Parallel genetic algorithms for large travelling salesrep problems. Master's thesis, University of Edinburgh, 1992.

Nix and Vose, 1991. A Nix and Michael D. Vose. Modeling genetic algorithms with markov chains. *Annals of Mathematics and Artificial Intelligence*, 5:79–88, 1991.

Radcliffe and George, 1993. Nicholas J. Radcliffe and Felicity A. W. George. A study in set recombination. In Stephanie Forrest, editor, *Proceedings of the Fifth International Conference on Genetic Algorithms*. Morgan Kaufmann (San Mateo, CA), 1993.

Radcliffe, 1990. Nicholas J. Radcliffe. *Genetic Neural Networks on MIMD Computers*. PhD thesis, University of Edinburgh, 1990.

Radcliffe, 1991a. Nicholas J. Radcliffe. Equivalence class analysis of genetic algorithms. *Complex Systems*, 5(2):183–205, 1991.

Radcliffe, 1991b. Nicholas J. Radcliffe. Forma analysis and random respectful recombination. In *Proceedings of the Fourth International Conference on Genetic Algorithms*, pages 222–229. Morgan Kaufmann (San Mateo), 1991.

Radcliffe, 1992a. Nicholas J. Radcliffe. Genetic set recombination. In Darrell Whitley, editor, *Foundations of Genetic Algorithms 2*. Morgan Kaufmann (San Mateo, CA), 1992.

Radcliffe, 1992b. Nicholas J. Radcliffe. Non-linear genetic representations. In R. Männer and B. Manderick, editors, *Parallel Problem Solving from Nature 2*, pages 259–268. Elsevier Science Publishers / North Holland (Amsterdam), 1992.

Radcliffe, 1993. Nicholas J. Radcliffe. Genetic set recombination and its application to neural network topology optimisation. *Neural Computing and Applications*, 1(1):67–90, 1993.

Shapcott, 1992. Jonathan Shapcott. Genetic algorithms for investment portfolio selection. Technical Report EPCC–SS92–24, Edinburgh Parallel Computing Centre, University of Edinburgh, 1992.

Spears and De Jong, 1991. William M. Spears and Kenneth A. De Jong. On the virtues of parameterised uniform crossover. In *Proceedings of the Fourth International Conference on Genetic Algorithms*, pages 230–236. Morgan Kaufmann (San Mateo), 1991.

Syswerda, 1989. Gilbert Syswerda. Uniform crossover in genetic algorithms. In *Proceedings of the Third International Conference on Genetic Algorithms*. Morgan Kaufmann (San Mateo), 1989.

Vose and Liepins, 1991a. Michael D. Vose and Gunar E. Liepins. Punctuated equilibria in genetic search. *Complex Systems*, 5:31–44, 1991.

Vose and Liepins, 1991b. Michael D. Vose and Gunar E. Liepins. Schema disruption. In *Proceedings of the Fourth International Conference on Genetic Algorithms*, pages 237–243. Morgan Kaufmann (San Mateo), 1991.

Vose, 1991. Michael D. Vose. Generalizing the notion of schema in genetic algorithms. *Artificial Intelligence*, 1991.

Whitley, 1992. Darrell Whitley. An executable model of a simple genetic algorithm. In Darrell Whitley, editor, *Foundations of Genetic Algorithms 2*. Morgan Kaufmann (San Mateo, CA), 1992.